

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 11:33:19 ; Search time 3431 Seconds

(without alignments)
15753.064 Million cell updates/sec

Title: US-09-718-754A-1

Perfect score: 1247

Sequence: 1 atcgcataaagtcgactt.....agagtcgctagcaactagca 1247

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_st:*
11: gb_sy:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
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31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119.2	9.6	7159	8	ZMA437281
2	116	9.3	6588	8	AY072300
3	108	8.7	6914	8	ZMA51453
4	106.8	8.6	6128	8	ZMA437282
5	102.4	8.2	9285	8	ZM009989
6	102.2	8.2	133080	2	AC146809
7	99.4	8.0	147198	8	AF466203
8	99	7.9	4695	6	A69563
9	99	7.9	4695	8	ZMPHYT1
10	98.6	7.9	183502	2	AC145227
11	97.8	7.8	6588	8	AY072300
12	97	7.8	226001	8	AF391808
13	92	7.4	135556	2	AC147603
14	88.4	7.1	113950	2	AC114395
15	88	6.3	318	6	AR252208
16	78.2	6.3	113950	2	AC114395
17	77.6	6.2	6506	8	AF434193
18	70.8	5.7	226001	8	AF391808
19	70.4	5.6	135556	2	AC147603
20	69.6	5.6	70679	2	AC147518
21	67.2	5.4	15783	8	AF347696
22	67.2	5.4	15783	8	AF347696
23	67.2	5.4	113950	2	AC114395
24	64.4	5.2	258658	3	AB014832
25	62.6	5.0	13868	6	AX027357
26	62.4	5.0	348600	1	AB063521
27	62.2	5.0	266371	2	AC020619
28	61.8	5.0	177650	9	AC104027
29	60	4.8	20063	8	CGP51533
30	59.8	4.8	110000	2	AC116984_3
31	58.8	4.7	181415	2	AC145262
32	58.4	4.7	349751	3	PFMAL4P3
33	58.2	4.7	1219	3	AF513853
34	58	4.7	5689	6	AX251180
35	58	4.7	5689	6	AX277927
36	58	4.7	5689	6	AX323612
37	57.8	4.6	854	9	HSU85253
38	57.8	4.6	1241	8	MITGVARI
39	57.4	4.6	340552	3	PFPA929354
40	57.2	4.6	105574	2	AC013308
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44	56.4	4.5	67970	3	PFMALIP3
45	56.4	4.5	169546	2	AC004157

ALIGNMENTS

RESULT 1
LOCUS ZMA437281 7159 bp DNA linear PLN 27-NOV-2003
DEFINITION Zea mays ZmEBE-1 gene for ZmEBE-1 protein, exons 1-5.
ACCESSION AJ437281
VERSION AJ437281.1 GI:28569665
KEYWORDS ZmEBE-1 gene; ZmEBE-1 protein.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 Magnard, J. L., Lehoucq, G., Massonneau, A., Heckel, T.,
Gutierrez-Marcos, J., Gomez, E., Perez, P., Dumas, C. and Rogowsky, P. M.

Pred. No. is the number of results predicted by chance to have a

FEATURES	source	location/Qualifiers
JOURNAL	embDDb and ZmDDb: two novel genes specifically expressed in the embryo sac and the basal endosperm transfer layer of maize	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 7159)	
TITLE	Rogowsky, P.M.	
JOURNAL	Direct Submission	
	Submitted (26-FEB-2002)	
	d'Italie, F-69364 Lyon Cedex 07, FRANCE	
	Location/Qualifiers	
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	/note="hybrid HD5XHD7"	
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	/gene="ZmEBE-1"	
	/number=1	
CDS	join(3596..3778, 4489..4668, 4742..4795, 4875..5012, 6181..6540)	
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	/number=1	
exon	4489..4668	
	/gene="ZmEBE-1"	
	/number=2	
intron	4669..4741	
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	/number=2	
exon	4742..4795	
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	/number=3	
intron	4796..4874	
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	/number=3	
exon	4875..5012	
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Matches 190; Conservative 0; Mismatches 68; Indels 10; Gaps 2;		
QY	263 CTAATCCAGATATTAGTAGAGATGTTAGTATAGAT-TAAGTGATGTTGAATGCACT 321	
Db	2362 CAACTCAAGTGTTGGGGGAGGTGTGATGATATGATGATAGGAGGTGTTGAATACACT 2421	
QY	322 AGAGCTAATATTGTGTAGCTAAATATTAGTTGAGACATCAACACCTA-----T 372	
Db	2422 AGAGCTAATATTGTGTAGCTAAATATTAGTTGAGACATCAACACCTTAACTTAAATAGTT 2481	

Query Match	Score	DB	Length
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LOCUS	AY072300
DEFINITION	Zea mays subsp. mays cytochrome P450 monooxygenase CYP72A5 gene, complete cds.
ACCESSION	AY072300
VERSION	AY072300.1
KEYWORDS	GI:21805644
SOURCE	Zea mays subsp. mays (maize)
ORGANISM	Zea mays subsp. mays
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 6588) Wang,J. and Schuler,M.A.
TITLE	Molecular characterization of the maize CYP71C3 and CYP72A subfamily genes
JOURNAL	2 (bases 1 to 6588) Wang,J., Reeds,R. and Schuler,M.A.
REFERENCE	Xenobiotics regulate maize cytochrome P450 monooxygenases at a post-transcriptional level
AUTHORS	Unpublished
TITLE	3 (bases 1 to 6588) Wang,J. and Schuler,M.A.
JOURNAL	Direct Submission
AUTHORS	Submitted (02-JAN-2002) Department of Cell and Structural Biology, University of Illinois at CU, 601 S. Goodwin Ave., Urbana, IL 61801, USA

Matches	190:	Conservative	0:	Mismatches	55:	Indels	11:	Gaps	3:
Qy	253	TTAATCACTACTAAATCCAGATATATTAGTAGAGATAGTATAGTATTAAGTATAGGTGATGTTT							312
Db	3397	TGAATGAAAGAAACGAAATAACGTTTATCTCCCTCACTCTTTAAGACTTAAGGGGGGTGTTT							3356
Qy	313	GAATGACATAGAGCTAATAGTATAGTACCTAAATAATAGTTGGAGACCTTCAACACCCCTA							371
Db	3357	GAATGACATAGAGATATAGTTAGTGGCTAGATTAAGTT-GAGACATCTCAACACCCCTAG							3415
Qy	372	-----TCAATTAATTAAGTATATTTTAAATTAATTAAGTATTAAGTATTAATTTAT							423
Db	3416	CTAATATAGTTCAGCTATAGCTATTTTGGTAAATATAGTAAATATAGTTAGTATTTGTT							3475
Qy	424	AAGTACTGTTTTTTTACTACGACATTTTAAAGCAACTAACAATTAAGTTTAACTATATCA							483
Db	3476	TAGCTAGCTAATTAATCTACTACACA-GTTTAAGCCAACTAATTAATTAAGTTCTAGTGCAITCA							3534
Qy	484	AATACCCCTAAGCGT	499						
Db	3535	AACACCCCTAATCCT	3550						
RESULT 3									
LOCUS	ZMA251453	6914 bp	DNA	linear	PLN	04-DEC-2000			
DEFINITION	Zea mays see2a gene for putative legumain, exons 1-9.								
ACCESSION	AJ251453								
VERSION	AJ251453.1	GI:11558851							
KEYWORDS	legumain; see2a gene.								
SOURCE	Zea mays								
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.								
REFERENCE	1	Donnison, I.S., Griffiths, C.M., Thomas, A., Hosken, S.E., Bridges, I. and Thomas, H.							
AUTHORS	Characterisation of See2, a senescence enhanced cDNA from maize with homology to legumain								
TITLE	Unpublished								
JOURNAL	2 (bases 1 to 6914)								
REFERENCE	Donnison, I.S.								
AUTHORS	Direct Submission								
TITLE	Submitted (03-DEC-1999) Donnison I.S., Cell Biology, Institute of Grassland & Environmental Research (IGER), Plas Gogerddan,								
JOURNAL	Aberystwyth, SY23 3EB, UNITED KINGDOM								
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	IFVYSYSHGGGVLGMPYRYLYGDDLDVLYKKRAATYKSLVLYLEACBSGSLFEG								
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	TESLKKOQKLVKDRPAVHDTPSYSGSHVYQGLLEINVRFLSYIGTDVANGNPFTED								
	NSTLSPKAVNORDADLYVFWOKRYKLADSSHAKREKRLLELVMAHSHYDVSVELI								
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[illegible]

Db 4100 T-TAAACATCCAAACATCATAGCTAATAGTATTAGTATTACTATTATTAGTAAATTAGT 4042

QY 402 TAAATGTTAGTATGTTATTTATAGTACTTTTATAGCAATTTTATAGCCAACTA 461

Db 4041 TAAATGTTAGTATGTTATTTATAGTACTTTATAGCAATTTTATAGCCAACTA 3983

QY 462 ACAATTAGTATTAGTATTCAATACC 489

Db 3982 ACTATTAGTCTTAATGATCAATCAACACC 3955

RESULT 4
ZMA437282 6128 bp DNA linear PIN 27-NOV-2003
LOCUS Zma mays ZmEBB-2 gene for ZmEBB-2 protein, exons 1-4.
ACCESSION AJ437282.1 GI:28569667
VERSION ZmEBB-2 gene; ZmEBB-2 protein.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Magnard,J.L., Lehouque,G., Massonneau,A., Heckel,T.,
Gutierrez-Marcos,J., Gomez,E., Perez,P., Dumas,C. and Rogowsky,P.M.
TITLE ZmEBB-2 gene and the basal endosperm transfer layer of maize
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6128)
AUTHORS Rogowsky,P.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2002) Rogowsky P.M., RDP, ENS-Lyon, 46 Allée
d'Italie, F-69364 Lyon Cedex 07, FRANCE
FEATURES
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ISFKIFKDKDDPMHIFGYDINNLIKPVGFPMKKSIFTNLDAGFITMGYTRSPNG
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intron
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intron

exon

ORIGIN

Query Match 8.6%; Score 106.8; DB 8; Length 6128;
Best Local Similarity 76.4%; Pred. No. 4.3e-14;
Matches 162; Conservative 0; Mismatches 37; Indels 13; Gaps 2;

QY 293 TATGATTAGGTGATGTTGATGCACAGCTAATAGTATTAGTAAATAGTTG 352

Db 5913 TAAGATTATGCGGTGTTGAATGATATAGAGCAATATAGTGGCTAAAAATAGTTG 5854

QY 353 GAGACATTCAAACACCCCA-----TCATTATTTAGTATTTTGTGTAATAGTTA 403

Db 5853 AAGACATCCAAACACTGCTAGCTAATAGTACGTATGCTATTTTGTGTAATAGTTA 5794

QY 404 ATAGT----TAGTGTATTATTATATAGCTAGCTTTTATCTAGCAATTTTATAGCCAAC 459

Db 5793 ATAGTGTAGTACTGATATTTGTAGTATAGCTATTTCTACTAGTATTTTATAGCAAT 5734

QY 460 TAACAATTAGTATTAGTATTCAATACCC 491

Db 5733 TAAATGTTAGTCTAGTACTTAAACACCTC 5702

RESULT 5
ZM009989 9285 bp DNA linear PIN 03-OCT-2002
LOCUS ZM009989
DEFINITION Zea mays D3L H(+) -transposing Atpase (Mha1) gene, complete cds.
ACCESSION U09989
VERSION U09989.1 GI:507770
KEYWORDS
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 2391 to 2453; 2525 to 2659; 2751 to 2930; 3019 to 3225;
3306 to 3425; 3510 to 3629; 3722 to 3844; 3927 to 3938)
AUTHORS Jin,Y.K. and Bennettzen,J.L.
TITLE Integration and nonrandom mutation of a plasma membrane proton
ATPase gene fragment within the Bgl retroelement of maize
JOURNAL Plant Cell 6 (8), 1177-1186 (1994)
MEDLINE 95003707
PUBMED 7919987
REFERENCE 2 (bases 1 to 9285)
AUTHORS Jin,Y.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1994) Young-Kwan Jin, Biological Sciences, Purdue
University, 339 Hansen Life Science Research Building, West
Lafayette, IN 47907, USA
FEATURES
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DEFINITION unorderd pieces.
ACCESSION AC146809.2 GI:38348713
VERSION HTG; HTGS_PHASE1; HTGS_FULFLOP; HTGS_ACTIVEFIN.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 133080)
Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bhatti,A.K.
and Messing,J.
Zea mays, clone ZMMBB0355F08
Unpublished
2 (bases 1 to 133080)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barua,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collamore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
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Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
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Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
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Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-OCT-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 133080)

```

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barua,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
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Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A., Zody,M.,
Butler,E., Wing,R., Bhatti,A.K. and Messing,J.

TITLE

JOURNAL

Submitted (26-NOV-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 16, 2003 this sequence version replaced gi:37574225.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIRB

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Bhatti, AK and Messing, J. The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(<http://pgr.rutgers.edu>)

Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

Project Information

Center project name: 355_P_8

Center clone name: 129774

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 83986 84085: gap of 100 bp
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* 119446 119545: gap of 100 bp
* 119546 128391: contig of 8846 bp in length
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FEATURES

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AUTHORS	1 (bases 1 to 147198)				
TITLE	laca.V, Linton.E.W., Young.S., Kovchok.S. and Messing.J.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (07-JAN-2002) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA				
AUTHORS	2 (bases 1 to 147198)				
TITLE	Ramakrishna.W., Samiguel,P., Emberton,J. and Bennetzen,J.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (07-JAN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA				
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repeat_region

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Best Local Similarity	71.3%; Pred. No. 3.2e-12;								
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Dd	27336 TTGACTAAGGGTGTCGTTAGATATACAGAATAATATGATCTGCTAAAATTAGCTGAA	27336							
Oy	335 GACATTTCAAACCCCTATCAAT-----TATTAGTTATTTTTAGTAAATTAGTTAT	405							
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RESULT 8									
A69563/c	4695 bp DNA linear PAT 07-MAY-1999								
LOCUS	A69563								
DEFINITION	Sequence 2 from Patent WO9805785.								
ACCESSION	A69563								
VERSION	A69563.1 GI:4774196								
KEYWORDS	.								
SOURCE	unidentified								
ORGANISM	unclassified.								
REFERENCE	1 (bases 1 to 4695)								
AUTHORS	Maugenest,S.; Perez,P. and Lescure,A.								
TITLE	PLANT PHYTASES AND BIOTECHNOLOGICAL APPLICATIONS								
JOURNAL	Patent: WO 9805785-A 2 12-FEB-1998; AGRONOMIQUE INST NAT RECH (FR) Other publication FR 2751987 19980206. Location/Qualifiers								
COMMENT									
FEATURES									
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ORIGIN									
Query Match	7.9%; Score 99; DB 6; Length 4695;								
Best Local Similarity	71.1%; Pred. No. 2.7e-12;								
Matches 167; Conservative 0; Mismatches 50; Indels 18; Gaps 2;									
Oy	272 AGATTATTAGTAGAGATGTTAGTATAGATTAAAGTGATGTTGAATGCACTAGACTAATA	331							
Dd	1307 AGTAGTTCCTCGATGACTAAATGGATTGAAGGGGTTATTGATGCACTAGACATATA	1248							
Oy	332 GTTAGTAGCTAAATTAAGTTGGAGACATTTAAACCCCTATCAAT-----	376							
Dd	1247 GT---TAGCTAAATTAAGTAGAGACATTTAAACCCCTATAGCTAATATATAGTTAGC	1191							

Oy		377	TATAGTAACTTTTAGTAATAATTAGTAACTAGTAACTGTTATTAATTAAGCAGCTTTT	436
Dd		1190	TATTACTAATTTTTAGTAATAATTAGCAGCTAGTCCTAGTAACTAATTTGGTAGTTAGTAAT	11311
Oy		437	TTACTAGCAATTTTTAGCCACACTAACAAATTAGTTAGTGATTAATCAATACCCC	491
Dd		1130	CTAGTATATATTTTACCTGACGTAACTAATTAGCTGTAGTGCATTCAAACAACC	1076
RESULT 9	ZMPHYTI/c			
LOCUS	ZMPHYTI	4695 bp	DNA	circular PLN 05-APR-1999
DEFINITION	Zea mays PHYT I gene for acidic phyase.			
ACCESSION	AJ223470			
VERSION	AJ223470.1 GI:3955064			
KEYWORDS	acidic phyase; PHYT I gene.			
SOURCE	Zea mays			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE	1			
AUTHORS	Maugeneet,S.; Martinez,I., Godin,B., Perez,P. and Leescure,A.M.			
TITLE	Structure of two maize phyase genes and their spatio-temporal expression during seedling development			
JOURNAL	Plant Mol. Biol. 39 (3), 503-514 (1999)			
MEDLINE	99190599			
PUBMED	10092178			
REFERENCE	2 (bases 1 to 4695)			
AUTHORS	Leescure,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-JUN-1998) lescure A., Laboratoire de biologie des semences, INRA, Route de saint Cyr, Versailles 78026 Cedex, FRANCE			
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Query Match	7.9%	Score 99	DB 8	Length 4695
Beat Local Similarity	71.1%	Pred. No. 2.7e-12		
Matches 167	Conservative 0	Mismatches 50	Indels 18	Gaps 2
OY	272	AGATATTAGTACAGATTGATATAGTATAGCTTAAGTGTGATGCTGACCTAGACTATA	331	
DB	1307	AGTGGTCCCTCGAGCTGACTAAATGGATTAAGGGGTTATTTGATGACCTAGAGATATA	1248	
OY	332	GTTAGTGCTAAATTTGTTGGACACATTCACACCCATTCATC-----	376	
DB	1247	GT---TAGCTAAATTTGCTAGACACATTCACACCCCTATAGCTAATATATAGTTAGC	1191	
OY	377	TATTAGTATTTTATAGTAATTAATAGTTATAGTTAGTTATTTATTAAGCTAGCTTTT	436	
DB	1190	TATTACATTTTATAGTAATTAATAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT	1131	
OY	437	TTACTAGCAATTTTATAGCCACCTAACAATTAAGTTAGTGTATTCAAATACCC	491	
DB	1130	CTACTAGCAATTTTATAGCTGACCTAAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT	1076	
RESULT 10				
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LOCUS				
DEFINITION				
AC145227.3	GI:37059943			
VERSION				
KEYWORDS	HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.			
SOURCE	Zea mays			
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				

Oy		304	GTAATGTTTGATGCACAGACGTAAATGTTAGTGGCTAAATAATTAGTTGAACAATTCAA	363
Dd		6243	GGCGTITTCGAATGCACAGAAGTCAATAGTTAGTTGCTAAAATTNGTTGAATATATCTCA	6184
Oy		364	ACACCCTA-----TCAATTATTAAGTATTTTTTACTGTAATAATTAGTTAAGTTACTTA	414
Dd		6183	ACATTGTATCTAAATAGTTCAACTATTAATTAAGTTACTTTAGTAAATATGTAATGTTGGCTA	6124
Oy		415	GTTATTTTAAAGCCTAGCTTTTTTTTACTAGCAATTTTTTAGCCACTAACATTAAGTTTTA	474
Dd		6123	GCTATTGTTGTAGCTCACTAAATTAATTATTAAGTATTAATTTTATAGCCAATTAAC---TAGCTCTA	6067
Oy		475	GTGATTTCAAAATACCCCTAAG	495
Dd		6066	GTACATTCAAACCCCTTAG	6046
RESULT 12				
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LOCUS	AF391808	226001 bp	DNA	linear
DEFINITION	Zea mays chromosome 9S bz genomic region strain MCC.			
ACCESSION	AF391808	AF296123	AF320086	X07940 Y00616
VERSION	AF391808.2	GI:17082476		
KEYWORDS	.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
AUTHORS	1 (bases 113967 to 117446)			
TITLE	Ralston,E.J., English,J.J. and Dooner,H.K. Sequence of three bronze alleles of maize and correlation with the genetic fine structure Genetics 119 (1), 185-197 (1988)			
JOURNAL MEDLINE	88284304			
PUBMED	3396861			
REFERENCE	2 (bases 118208 to 122429) Shen,B., Zheng,Z. and Dooner,H.K. A maize sesquiterpene cyclase gene induced by insect herbivory and volicitin: characterization of wild-type and mutant alleles Proc. Natl. Acad. Sci. U.S.A. 97 (26), 14807-14812 (2000)			
AUTHORS	Fu,H., Park,W., Yan,X., Zheng,Z., Shen,B. and Dooner,H.K. The highly recombinogenic bz locus lies in an unusually gene-rich region of the maize genome Proc. Natl. Acad. Sci. U.S.A. 98 (15), 8903-8908 (2001)			
TITLE	3 (bases 91198 to 151800) Fu,H., Zheng,Z. and Dooner,H.K. Recombination rates between adjacent genic and retrotransposon regions in maize vary by 2 orders of magnitude Proc. Natl. Acad. Sci. U.S.A. 99 (2), 1082-1087 (2002)			
JOURNAL MEDLINE	21664393			
PUBMED	11792865			
REFERENCE	5 (bases 127678 to 226001) Fu,H. and Dooner,H.K. From the Cover: Intraspecific violation of genetic colinearity and its implications in maize Proc. Natl. Acad. Sci. U.S.A. 99 (14), 9573-9578 (2002)			
AUTHORS	Fu,H., Zheng,Z. and Dooner,H.K. Direct Submission Submitted (15-JUN-2001) Waksman Institute, Rutgers University, 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA 7 (bases 1 to 226001) Fu,H., Shen,B., Ralston,E.J., Zheng,Z. and Dooner,H.K. Direct Submission			
JOURNAL MEDLINE	22103619			
PUBMED	12060715			
REFERENCE	6 (bases 1 to 226001) Fu,H., Zheng,Z. and Dooner,H.K. Direct Submission Submitted (15-JUN-2001) Waksman Institute, Rutgers University, 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA 7 (bases 1 to 226001) Fu,H., Shen,B., Ralston,E.J., Zheng,Z. and Dooner,H.K. Direct Submission			
AUTHORS				
TITLE				

FEATURES	Source
JOURNAL	Submitted (26-NOV-2001) Wakeman Institute, Rutgers University, 190 Frelinghuysen Rd, Piscataway, NJ 08854, USA
REMARK	Sequence update by submitter
COMMENT	On or before Nov 26, 2001 this sequence version replaced gi:22204, gi:11545432, gi:13241666, gi:14719277.
FEATURES	Location/Qualifiers
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Oy	644	GGCGTCTCTAAGAAACCGCCCGGTGTCTAAGATATTTCACCTAGCGGTGGTGACAACACT	703
Db	21493	GGT-TCCTTTAAGAAACCGCCAGTGAACCGCACTTTTCACTGGCGGTTCCAAATAACCC	21435
Oy	704	GCCTGTGAAAAAACCGCATTCCTATCTAGCCCTTAGCTGTGACCTGGGACATAAAAACGT	763
Db	21434	GCCAGTGC-GAATATCTATTTTTCACATCAACCCCTTAGC---ACTGCGGTACTGAAAAACGC	21375
Oy	764	CAGTGAATAATAGCTCTTAGCATTCGTCACTATAGAGCTTCTATGTACT	809
Db	21378	CAGTGAATAATAGCTTTTAGAACCGCCCACTATAGAGCTTCTGTGTACT	21333
RESULT 15			
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LOCUS			
DEFINITION			
ACCESSION	AC146809	133080 bp	DNA
VERSION	AC146809.2		GI:38348713
KEYWORDS	HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.		
SOURCE	Zea mays		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE			
AUTHORS	Bliren,B., Nusbäum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K. and Messing,J.		
TITLE	Zea mays clone ZMMBB0355F08		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 133080)		
AUTHORS	Bliren,B., Nusbäum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Atrashchi,H.M., Barna,N., Baetien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Cornu,B., DeArliano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gadyana,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karacas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., McLean,C., McDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrum,J., Menues,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nuygen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rechupka,A., Ramasamy,U., Raymond,C., Retta,R., Rice,C., Rogov,P., Roman,J., Schauer,S., Schnuppck,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talanas,J., Teste,S., Theodore,U., Topham,K., Travers,M., Vassiliiev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 133080)		
AUTHORS	Bliren,B., Nusbäum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Atrashchi,H.M., Barna,N., Baetien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Cornu,B., DeArliano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gadyana,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karacas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., McLean,C., McDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrum,J., Menues,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,		

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TITLE
JOURNAL

COMMENT
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Neway, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunhkhong, P., Pierre, N.,
Rachpaka, A., Ramasamy, U., Raymond, C., Retta, R., Rice, C., Rogov, P.,
Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Zody, M.,
Butler, E., Wing, R., Bharti, A.K. and Messing, J.
Direct Submission
Submitted (26-NOV-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 16, 2003 this sequence version replaced gi:37574225.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Bharti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(http://pgr.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
-----
Project Information
Center project name: L29774
Center clone name: 355_F_8
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 83985: contig of 83985 bp in length
* 83986 84085: gap of 100 bp
* 84086 119445: contig of 35360 bp in length
* 119446 119545: gap of 100 bp
* 119546 128391: contig of 8846 bp in length
* 128392 128491: gap of 100 bp
* 128492 130558: contig of 2067 bp in length
* 130559 130658: gap of 100 bp
* 130659 133080: contig of 2422 bp in length.
*
Location/Qualifiers
1. 133080
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/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4577"
/clone="ZM8B0355F08"
/clone_lib="CUGI HindIII BAC Library"

FEATURES
source
Query Match 7.1%; Score 88; DB 2; Length 133080;
Best Local Similarity 65.4%; Pred. No. 1.4e-09;
Matches 191; Conservative 0; Mismatches 95; Indels 6; Gaps 4;

ORIGIN
Dy 518 GAATCTTAACCGAATGTGAGACACATTTTCATAGTGCTACTGTTTAAGTACGCTGAC 577
Db 77810 GAAAAATTTAAAAAAGCGCGGAAAACTTTCCACTGCGCACTAAATAAAAAACAACGCGCG 77751
Oy 578 TGATAATTAATTTTACACATGCGGTTCTTTAAGCAAAACGCGAGTGCTAATGATATTAC 637
Db 77750 TGGAAATAGCATTTCCAC-TCGGTTTTCTTAATTAATAAACCGCAAGTGGAATAGCATTTTC 77692

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77576 AAGCGCAGTGAACGCTCTAGAACCGCACTATAGAGGCTGTGTACT 77525

Completed: July 17, 2004, 13:32:45
 : 3437 BECS

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 10:30:44 ; Search time 413 Seconds
(without alignments)
12826.884 Million cell updates/sec

Title: US-09-718-754a-1

Perfect score: 1247

Sequence: 1 atcgacataaagtgtgact.....agagtcgctgacactagca 1247

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002s:*
7: geneeqn2003as:*
8: geneeqn2003bs:*
9: geneeqn2003cs:*
10: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1247	100.0	1247	6	AAD43992
2	119.2	9.6	3598	6	ABN85030 Maize jip
3	108.4	8.7	9824	2	ACA62291 Maize pro
4	104.6	8.4	925	8	ACA62291 Maize pro
5	99	7.9	4695	2	AAV49471 Maize phy
6	78.2	6.3	318	7	ABX89107 Corn ear-
7	62.6	5.0	13868	3	AA51324 Z. mays M
8	58	4.7	5689	4	AA545384 Chemical
9	58	4.7	5689	4	AA545384 Chemical
10	58	4.7	5689	6	ABK28226 Tumour su
11	56.2	4.5	2000	7	ADA71938 Rice gene
12	56	4.5	10286	4	AA545309 Chemical
13	56	4.5	10286	6	ABK28148 DNA trans
14	55.2	4.4	6219	6	ABK28148 DNA trans
15	55.2	4.4	6219	6	AA563324 Chemical
16	54	4.3	14987	6	ABK32631 Human imm
17	52.2	4.2	110000	7	AA53224_2 Continuation (3 of
18	51.8	4.2	24939	6	ABL70570 Chemical
19	51.4	4.1	33053	6	ABQ67006 Human ang
20	50.2	4.0	12142	6	ABK32673 Human imm
21	50.2	4.0	14924	6	ABK32225 Human imm
22	50.2	4.0	14924	6	ABK54332 Chemical
23	50	4.0	15714	6	ABK33172 Human imm

24	50	4.0	15714	6	ABQ67057 Human ang
25	49.8	4.0	925	8	ACA62291 Maize pro
26	49.8	4.0	8576	6	ABK34228 Human imm
27	49.6	4.0	6541	6	ABK32314 Human imm
28	49.6	4.0	6641	6	ABK54335 Chemical
29	49.6	4.0	9824	2	AAQ40763 Wild-type
30	49.4	4.0	6464	6	ABK32514 Human imm
31	49.4	4.0	6585	6	ABK32833 Human imm
32	49.4	4.0	6585	6	AA61183 Human gen
33	49.4	4.0	8056	7	ABK10246 Haematopo
34	49.2	3.9	8056	7	ABK10246 Haematopo
35	49.2	3.9	8305	6	ABK33568 Human imm
36	49	3.9	71843	7	ACC79619 Zebrafish
37	48.6	3.9	3991	4	AA616633 Human nov
38	48.6	3.9	3991	9	AA62077 Human sec
39	48.6	3.9	14798	6	ABK33033 Human imm
40	48.4	3.9	6123	6	ABK32820 Human imm
41	48.4	3.9	26997	4	AA546747 Tumour su
42	48.4	3.9	271990	9	ADD25213 Fertilicy
43	48.2	3.9	17674	6	ABK33345 Human imm
44	48	3.8	5520	6	ABK33518 Human imm
45	47.8	3.8	6160	6	ABK33533 Human imm

ALIGNMENTS

RESULT 1	AAD43992	standard; DNA; 1247 BP.
ID	AAD43992	
XX		
AC	AAD43992:	
XX		
DT	13-DEC-2002	(first entry)
XX		
DE	Maize jip1 promoter DNA.	
XX		
KW	Regulatory element; maize jip1; maize mlpb3; maize lecl;	
KW	exogenous product; endogenous product; de.	
XX		
OS	Zea mays.	
XX		
FH	Key	Location/Qualifiers
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FT	FT	/*tag= a
FT	TATA_signal	801..885
FT	FT	/*tag= b
XX		
PN	WO200242424-A2.	
XX		
PD	30-MAY-2002.	
XX		
PF	20-NOV-2001; 2001WO-US044732.	
XX		
PR	22-NOV-2000; 2000US-00718754.	
XX		
PA	(PION-) PIONEER HI-BRED INT. INC.	
PI	Lappegard KK, Abdlit SE, Martino-Catt SJ, Shi J, Gordon-Kamm WJ;	
PI	Lowe KS;	
XX		
DR	WPI; 2002-463629/49.	
XX		
PT	New regulatory element, useful for controlling the expression of	
PT	endogenous as well as exogenous products in a seed-preferred manner.	
XX		
PS	Claim 1, Page 40-41; 46pp; English:	
XX		
CC	The invention relates to an isolated regulatory element capable of	
CC	driving transcription in seed-preferred manner comprising sequences	
CC	natively associated with DNA coding for maize jip1; maize mlpb3 or maize	
CC	lecl. The method is useful for selectively expressing a nucleotide	
CC	sequence in a plant seed, by transforming a plant cell with transformed	

CC vector. The invention are useful for controlling the expression of
CC endogenous as well as exogenous products in a seed-preferred manner. The
CC present sequence is maize jipl promoter DNA

XX Sequence 1247 BP; 400 A; 240 C; 249 G; 358 T; 0 U; 0 Other;

Query Match 100.0%; Score 1247; DB 6; Length 1247;
Best Local Similarity 100.0%; Pred. No. 3.2e-295;
Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATCGTCATTAAGTGGATTATATCAATTCATTTCAACTAAATGAAACCAATTAAT 60
DB 1 ATCGTCATTAAGTGGATTATATCAATTCATTTCAACTAAATGAAACCAATTAAT 60
QY 61 TAAAAAATCAAAAAAACCCTTTATCAACCGTACAGAGAAAGAGACATCACTTGCCTATAG 120
DB 61 TAAAAAATCAAAAAAACCCTTTATCAACCGTACAGAGAAAGAGACATCACTTGCCTATAG 120
QY 121 TTTTATGATTTAAACACCCCTTGAACCATCAAGACAGTGGTTGATAGTTTAACTGATCT 180
DB 121 TTTTATGATTTAAACACCCCTTGAACCATCAAGACAGTGGTTGATAGTTTAACTGATCT 180
QY 181 AATATCTTGTCTTTATATCTAGACCAACTGATTAATCTTCCACACATGTTATAT 240
DB 181 AATATCTTGTCTTTATATCTAGACCAACTGATTAATCTTCCACACATGTTATAT 240
QY 241 CTATTGTGACTTATCAATTAATCAAGATTTAGTAGATGTTAGTATGATT 300
DB 241 CTATTGTGACTTATCAATTAATCAAGATTTAGTAGATGTTAGTATGATT 300
QY 301 AAGGTGATGTTGAATGACACTAGAGCTAAATAGTACGTAATTAATAGTTGAGACATT 360
DB 301 AAGGTGATGTTGAATGACACTAGAGCTAAATAGTACGTAATTAATAGTTGAGACATT 360
QY 361 CAACACCCCTATCAATTAATAGTATTTTATAGTAAATAGTAAATAGTAAATAGTAAAT 420
DB 361 CAACACCCCTATCAATTAATAGTATTTTATAGTAAATAGTAAATAGTAAATAGTAAAT 420
QY 421 TTTAAGCTGCTTTTATCTAGACATTTTATGACCACTAACTAATAGTTAGTAT 480
DB 421 TTTAAGCTGCTTTTATCTAGACATTTTATGACCACTAACTAATAGTTAGTAT 480
QY 481 TCMAATACCCCTTAAGCCGTTAAGTATGCTCTTTCTAGAATCTTAAACGATGTGAGAC 540
DB 481 TCMAATACCCCTTAAGCCGTTAAGTATGCTCTTTCTAGAATCTTAAACGATGTGAGAC 540
QY 541 AACATTTTATAGGTGATCTGTTTAAAGTCAACGCTCATGATTAATATATTTTCACTGCG 600
DB 541 AACATTTTATAGGTGATCTGTTTAAAGTCAACGCTCATGATTAATATATTTTCACTGCG 600
QY 601 GTTCTTAAGCAACGCCAGTGTCTAATATTTACCTAGCGGCGCTGTAAGAAAC 660
DB 601 GTTCTTAAGCAACGCCAGTGTCTAATATTTACCTAGCGGCGCTGTAAGAAAC 660
QY 661 CGCCCGTCTAAAGATATTTTACCTAGCGGTTGTAACAACCTGCTGTAAGAAACCGG 720
DB 661 CGCCCGTCTAAAGATATTTTACCTAGCGGTTGTAACAACCTGCTGTAAGAAACCGG 720
QY 721 ATTCTACTAGCCCTAGCTTGACCTGGGACATTAATAAAGCTCACTGTAATAGCTCTA 780
DB 721 ATTCTACTAGCCCTAGCTTGACCTGGGACATTAATAAAGCTCACTGTAATAGCTCTA 780
QY 781 GGATCGTCACTAAGAGCTTCTATGTAAGTGTAGAGATGATTTGATGTGACCA 840
DB 781 GGATCGTCACTAAGAGCTTCTATGTAAGTGTAGAGATGATTTGATGTGACCA 840
QY 841 AGTGCAGATTTTAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
DB 841 AGTGCAGATTTTAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
QY 901 CGATTTCTATAGTATGTTGCTTGCAAGCCGAAATAGATTAACATTTGCTGTCACAG 960
DB 901 CGATTTCTATAGTATGTTGCTTGCAAGCCGAAATAGATTAACATTTGCTGTCACAG 960

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QY 961 AATCCACATTAATCAAGTTCATGCGCGCCGACAGTACCAATCCACGCTGCTG 1020
DB 961 AATCCACATTAATCAAGTTCATGCGCGCCGACAGTACCAATCCACGCTGCTG 1020
QY 1021 CGGAGACACGCTGTTGCTGACCGGACATTTGGCCGATACACATGACACAGCCGAGCA 1080
DB 1021 CGGAGACACGCTGTTGCTGACCGGACATTTGGCCGATACACATGACACAGCCGAGCA 1080
QY 1081 ATAGAAGAAAGACGACGACGCGCGGACACCGCCGATAGTATGATGATGATGATGATGAT 1140
DB 1081 ATAGAAGAAAGACGACGACGCGCGGACACCGCCGATAGTATGATGATGATGATGATGAT 1140
QY 1141 TGTAGCTTTTTCAGAGCGCTGCTGTAATACTAGACCTTTCCACAGCGAGGAGG 1200
DB 1141 TGTAGCTTTTTCAGAGCGCTGCTGTAATACTAGACCTTTCCACAGCGAGGAGG 1200
QY 1201 GGGAGAGATATCTGCTAGTACGACAGAGAGAGTGGCTAGCACTAGCA 1247
DB 1201 GGGAGAGATATCTGCTAGTACGACAGAGAGAGTGGCTAGCACTAGCA 1247

```

RESULT 2

```

ABN85030
ID ABN85030 standard; DNA; 3598 BP.
XX
AC ABN85030;
XX
DT 27-SEP-2002 (first entry)
XX
DE Maize DD1-a promoter.
XX
KM Plant; maize; DD1-a; DD1-b; seed transfer zone; transgenic plant;
XX promoter; chromosome 8q; ds.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT TATA_signal 3518..3524
FT /*tag= a
XX
PN WO200236788-A2.
XX
PD 10-MAY-2002.
XX
PF 06-NOV-2001; 2001WO-FR003439.
XX
PR 06-NOV-2000; 2000FR-00014214.
XX
PR 19-DEC-2000; 2000FR-00016602.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA (CNRS ) CENT NAT RECH SCI.
PA (ECOL-) ECOLE NORMALE SUPERIEURE DE LYON.
PA (UYLY-) UNIV LYON I BERNARD CLAUDE.
XX
PI Rogowsky P, Magnard J, Perez P;
XX
DR MPI; 2002-519253/55.
XX
PT New DD1-a and DD1-b genes of maize and their regulators, useful for
PT specific control of transgene expression in the transfer zone of grain
PT during development.
XX
PS Claim 2, Fig 5; 140pp; French.
XX
CC The present sequence is the promoter of maize DD1-a gene. The DD1-a and
CC DD1-b genes are expressed specifically in the transfer zone of the seed
CC during development. They are used to prepare transgenic plants,
CC particularly where their regulatory regions are used to control a wide
CC variety of genes of interest, especially genes that improve agronomic,
CC nutritional or industrial quality. The DD1 genes may also be used for
CC recombinant expression of DD1 proteins, overexpression of which may
CC increase quantity and/or quality of metabolites in the ripe grain and

```

CC Improve resistance to various pathogens. The DDI-a gene is located on
 CC maize chromosome 8q
 XX
 SQ Sequence 3598 BP; 1022 A; 738 C; 739 G; 1098 T; 0 U; 1 Other;
 Query Match 9.6%; Score 119.2; DB 6; Length 3598;
 Best Local Similarity 70.9%; Pred. No. 6.5e-19;
 Matches 190; Conservative 0; Mismatches 68; Indels 10; Gaps 2;
 OY 263 CTAAATCCAGATATTAGTAGAGATGTAGTATAGAT-TAGAGTATGTTTGAATGCACT 321
 DB 2362 CAACCTCAAGTGTGGGGAGTTGTGAGTAAAGTAGTAGGGGTGTTGAATACACT 2421
 OY 322 AGAGCTAATAGTTAGTAGCTAAATAGTTGAGACATCAACACCCCTA-----T 372
 DB 2422 AGAGCTAATAGTTAGTAGCTAAATAGTTGAGACATCTAAACACTCTAGTTAATAGTT 2481
 OY 373 CAATTATAGTTATTTTATAGTAATAGTTAATAGTTAGTTATTTATTAAGTAGCT 432
 DB 2482 CAACATATAGCTATTTTATAGTAATAGTTAATAGTTAGTTAGTTAGTTAGTT 2541
 OY 433 TTTTCTACTAGCAATTTTATAGCACTAACAATTGCTTTAGTGTATTCAAATACCCCT 492
 DB 2542 AATTCACCTAGCAAAATTTTATAGCACTAACAATTAGTGTGAGTGCATTCACACCCCTAA 2601
 OY 493 AAGCCGTTAAGTAGTCTCTTTCTAGAA 520
 DB 2602 AGAAGATGGACACGATCTAGCGGTA 2629
 RESULT 3
 AAQ40763/c
 ID AAQ40763 standard; DNA; 9824 BP.
 XX
 AC AAQ40763;
 XX
 DT 25-MAR-2003 (revised)
 XX
 DT 14-SEP-1993 (first entry)
 XX
 DE Wild-type shrunken-2 gene.
 XX
 KW Wild-type; shrunken-2; Sh-2; gene; plasmid; replication; Bt-2; starch;
 sequencing; ADP-glucose pyrophosphorylase; ADP-GPP; cloning; sucrose;
 brittle-2; ADP-glucose; pyrophosphate; ATP; sh-2; bt-2; hydrolysis;
 KW glucose-1-phosphate; chain elongation; starch synthetase; homozygous;
 recessive; supersweet; corn; ss.
 XX
 KW Zea mays.
 XX
 OS
 XX
 PN WO9309237-A1.
 XX
 PD 13-MAY-1993.
 XX
 PF 04-NOV-1992; 92WO-EP002531.
 XX
 PF 05-NOV-1991; 91US-00791933.
 XX
 PR (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ LTD.
 XX
 PI Nichols SE, Pauly MH, Sinibaldi RM, Weeks DP, Baker FC;
 PI Duncan ML;
 XX
 DR WPI; 1993-167702/20.
 XX
 PT Super-sweet corn plants and seed - have sweet or starchy kernels at
 PT harvest for food or seed, respectively.
 XX
 PS Claim 23; Page 30-36; 49pp; English.
 XX
 CC This sequence represents the wild-type shrunken-2 (Sh-2) gene. The Sh-2
 CC gene contains a sequence which interferes with plasmid replication which

CC caused difficulties in cloning and sequencing the Sh-2 gene. The Sh-2
 CC gene encodes a 60 kD protein which is involved in starch production. The
 CC Sh-2 protein represents two subunits of the four subunit enzyme ADP-
 CC glucose pyrophosphorylase (ADP-GPP). The other two subunits of ADP-GPP
 CC comprise a 55 kD polypeptide encoded by the brittle-2 (Bt-2) gene. ADP-
 CC GPP catalyses the reversible synthesis of ADP-glucose and pyrophosphate
 CC from ATP and glucose-1-phosphate. The reaction is driven by pyrophosphate
 CC hydrolysis. ADP-glucose is the glucosyl donor for starch chain elongation
 CC catalysed by starch synthetase. When either the Sh-2 or Bt-2 gene is
 CC present in the homozygous recessive state (Sh-2 or Bt-2 respectively) the
 CC 60 kD or 55kD subunits respectively are not synthesised and little or no
 CC functional ADP-GPP is made. Therefore starch synthesis is impaired,
 CC sucrose accumulates to 2-4 times the levels of normal sweet corn and the
 CC result is "supersweet" corn. (updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 9824 BP; 2718 A; 1910 C; 1915 G; 3281 T; 0 U; 0 Other;
 Query Match 8.7%; Score 108.4; DB 2; Length 9824;
 Best Local Similarity 75.2%; Pred. No. 4e-16;
 Matches 152; Conservative 0; Mismatches 41; Indels 9; Gaps 1;
 OY 297 GATTAAAGTGATGTTGAATGCACTAGAGCTAATAGTTAGTACCTAAATAGTTGAGA 356
 DB 9541 GACTTAAGGGGTGTTGAATGCAATAGAGCTAATAGTTAGTTAAATAGTCTGAAGA 9482
 OY 357 CATTCAAAACACCTA-----TCAATTATAGTTATTTTATAGTAATAGTTAATAG 407
 DB 9481 CATCTAAACAAATATAGCTAATAGTTACAGCTATATGCTATTTTAAACAAATAGCTAATAG 9422
 OY 408 TTAGTTAGTTATTTTAAAGCTAGCTTTTCTTCTAGCAATTTTATAGCACTAACAATTG 467
 DB 9421 TTAGCTAGCTATTTTGTAGCTAGCTAATTTTCAAGTCAATTTTGTGTCAACTAATATT 9362
 OY 468 AGTTTATAGTATTCAAATACC 489
 DB 9361 AGCTCTAATGATTTTAAACACC 9340
 RESULT 4
 ACA62291/c
 ID ACA62291 standard; DNA; 925 BP.
 XX
 AC ACA62291;
 XX
 AC 12-AUG-2003 (first entry)
 XX
 DT
 XX
 DE Maize proteinase inhibitor gene, promoter.
 XX
 KW Maize; ds; promoter; proteinase inhibitor; plant; development;
 KW developmental pathway; plant defence response; disease resistance.
 XX
 OS
 XX
 PN US200303632-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 23-OCT-2001; 2001US-00039836.
 XX
 PF 25-OCT-2000; 2000US-0243167P.
 XX
 PR (PION-) PIONEER HI-BRED INT INC.
 XX
 PA Crane VC, Simmons CR;
 XX
 PI WPI; 2003-466274/44.
 XX
 DR
 XX
 PT New maize proteinase inhibitor-like polypeptide and polynucleotides
 PT useful in expression cassettes for modulating development, developmental
 PT pathways, and plant defense response, and for enhancing disease
 PT resistance in plants.
 XX

PS Claim 7; Page 26; 29pp; English.

XX
CC The invention relates to a new isolated polypeptide comprising: (a) the
CC maize proteinase inhibitor appearing as ABU61637; (b) a sequence encoded
CC by the nucleotide sequence appearing as ACA62290, or by the cDNA insert
CC deposited as Patent Deposit Number not given in the specification; (c) at
CC least 75% identity to ABU61637, where the polypeptide has proteinase
CC inhibitor-like activity; or (d) at least 20 contiguous amino acids of
CC ABU61637. Also included are an isolated nucleic acid molecule
CC (comprising, or having at least 75% sequence identity to or at least 20
CC contiguous nucleotides of ACA62290 encoding ABU61637, or hybridising
CC under stringent conditions in 50% formamide, 1 M NaCl, 1% sodium dodecyl
CC sulphate (SDS) at 37 pluso C and a wash in 0.1% saline sodium citrate
CC (SSC) at 60-65 pluso C to the complement of the above sequences), a DNA
CC construct comprising the nucleic acid molecule operably linked to a
CC promoter that drives expression in the host cell, a vector comprising the
CC DNA construct, a plant cell comprising the vector, a plant having stably
CC incorporated into its genome at least one of the DNA constructs cited
CC above, a method for modulating disease resistance in plant by stably
CC introducing into the genome of the plant at least one of the DNA
CC construct comprising a heterologous promoter active in the plant, a
CC method for modulating the level of a polypeptide in a plant (by
CC introducing into the genome of the plant cell a DNA construct comprising
CC the polynucleotide operably linked to a promoter, culturing the plant
CC cell under plant growing conditions to produce a regenerated plant, and
CC inducing expression of the polynucleotide for a time sufficient to
CC modulate the level of the polypeptide in the plant) and a method for
CC regulating the expression of a nucleotide sequence of interest (by stably
CC incorporating into the genome of a plant cell a nucleotide sequence of
CC interest operably linked to the promoter cited above. The polypeptide,
CC polynucleotides and methods are useful in expression cassettes for
CC modulating development, developmental pathways, and plant defence
CC response, and for enhancing disease resistance in plants. The present
CC sequence represents the promoter from the maize proteinase inhibitor
CC gene which may be used in the DNA constructs cited above for expressing a
CC gene of interest
XX
SQ Sequence 925 BP; 258 A; 178 C; 202 G; 287 T; 0 U; 0 Other;

Query Match 8.4%; Score 104.6; DB 8; Length 925;

Best Local Similarity 79.7%; Pred. No. 1.5e-15; Mismatches 29; Indels 13; Gaps 3;

Matches 165; Conservative 0; Mismatches 29; Indels 13; Gaps 3;

OY 295 TAGATTAAAGTATGTTGAATGACTAGAGCTAATAGTAGTAAATTAAGTGA 354
DB 465 TAGACTTATGACATGTTTGAATGACTAAGATAAAGTTAGTGAATTAAGTT-GA 407
OY 355 GACATTCAAAACACCTATC-----AATTATTAGTTATTTTGAATAATTAGTTAA 404
DB 406 GACATTCAAAACAGCCCACTTAATTAATTAAGTTATTTTGGTAATAATTAGTTAA 347
OY 405 TAGTTAGTATGTTATTTTAACTAGCTTTTCTTACTAGCAATTTTTCGCCAATAACA 464
DB 346 TAGTTAGTATGTTATTTTAACTAGCTTTTCTTACTAGCAATTTTTCGCCAATAACT 289
OY 465 ATTAGTTTATGTTATTTTCAATACCC 491
DB 288 ATTAGTTTATGTTATTTTCAATACCC 262

RESULT 5

AAV49471/C ID AAV49471 standard; cDNA; 4695 BP.

XX AAV49471;

XX 10-NOV-1998 (first entry)

DE Maize phyase genomic clone P19.14.

XX Maize; phyase; PCR; amplification; primer; probe; hybridisation;
KW transgenic plant; starch; seed; nutrition; cereal; steep liquor; ss.
XX

OS Zea mays.

XX Key Location/Qualifiers

PH prim_transcript 1935..3403

FT /tag= a

FT exon 1935..1947

FT /tag= b

FT intron 1948..2078

FT /tag= c

FT exon 2079..3403

FT /tag= d

FT CDS 2097..3260

FT /tag= e

FT /product= "phyase"

XX FR2751987-A1.

XX 06-FEB-1998.

XX 01-AUG-1996; 96FR-00009734.

XX 01-AUG-1996; 96FR-00009734.

XX (BIOC-) BIOCEM SA.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Perez P, Maugenest S, Lescure AM;

XX WPI; 1998-133139/13.

XX P-PSDB; AAW49696.

PT DNA encoding maize phyase enzyme - useful for producing recombinant

PT phyase or transgenic plants with increased phyase levels.

XX Claim 9; Fig 4; 67pp; French.

PS This sequence represents the sequence of a genomic clone (P19.14)

CC encoding a maize phyase protein. The sequence was isolated from a maize

CC genomic DNA library screened with the phyase cDNA sequence (AAV49470).

CC From 13 clones isolated from the library, 2 classes of clones were

CC obtained based on their restriction maps. This sequence belongs to the

CC class I clones and has been located on the short arm of chromosome 3

CC between loci umc010 and umc026. The phyase sequence can be used to

CC generate transgenic plants for production of a high level of phyase. The

CC phyase, or seeds containing it, are used to extract starch from plant

CC seeds, especially for increasing the nutritive quality of e.g. cereals,

CC and/or to upgrade steep liquors

SQ Sequence 4695 BP; 1347 A; 1021 C; 1013 G; 1314 T; 0 U; 0 Other;

Query Match 7.9%; Score 99; DB 2; Length 4695;

Best Local Similarity 71.1%; Pred. No. 6.3e-14; Mismatches 50; Indels 18; Gaps 2;

Matches 167; Conservative 0; Mismatches 50; Indels 18; Gaps 2;

OY 272 AGATTATGTTGAGATGTTAGTATGATTAAGGTGATGTTGAATGACTAGACTATA 331
DB 1307 AGTAGTCTCGAGGACTAAATGGATTAAGGGGTTATTGAATGACTAGAGATAATA 1248
OY 332 GTTAGTAAATTAAGTTGAGACATTTCAACACCCCTATCAAT----- 376
DB 1247 GT---TAGTAAATTAAGTGAAGACATCAACACCCCTATGCAATATATATAGTTAGC 1191
OY 377 TATTAGTATTTTATGTAATTAAGTTAATGTTAGTTATTTTATTAAGCTAGCTTTT 436
DB 1130 TATTAGTATTTTATGTAATTAAGTTAATGTTAGTTATTTTATTAAGCTAGCTTTT 1131
OY 437 TTACTAGCAATTTTATGCAATTAAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTT 491
DB 1130 CTACTAGTATATTTTATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1076

RESULT 6
ABX89107 ID ABX89107 standard; cDNA, 318 BP.
XX AC ABX89107;
XX DT 24-APR-2003 (first entry)
XX DE Corn ear-derived polynucleotide (cpd) #7567.
XX CM Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
XX CM structural gene; functional gene; regulatory gene;
XX CM corn ear-specific profile; gene transcription; gene expression;
XX CM hybrid plant; desirable trait expression; plant breeding program;
XX CM inheritance; desired characteristic; growth; development;
XX CM disease resistance; environmental adaptability; quality; yield;
XX CM multigene trait; plant; gene; ss.
XX OS Zea mays.
XX PN US6476212-B1.
XX PD 05-NOV-2002.
XX PF 14-MAY-1999; 99US-00313294.
XX PR 26-MAY-1998; 98US-0086722P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Laigudi RV, Ito LY, Sherman BK;
XX WP; 2003-208840/20.
XX PT Novel purified corn-ear derived polynucleotide useful as hybridization
PT probe for detecting polynucleotide in sample, and for identifying,
PT evaluating, and altering desired characteristics associated with growth,
PT development.
XX PS Example; SEQ ID NO 7567; 390pp; English.
XX CC The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and SATMON023. Some of the cdfs uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotide sequences are
CC useful for detecting cdfs in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC hybrid or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cdfs are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridization techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cdfs are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth,
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cdfs are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cdfs are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived
CC polynucleotides (cdfs) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipaididentity.html
XX SQ Sequence 318 BP; 90 A; 65 C; 54 G; 97 T; 0 U; 12 Other;
XX QY Query March 6.3%; Score 78.2; DB 7; Length 318;
XX BL Best Local Similarity 82.6%; Pred. No.3.1e-09;
XX MA Matches 100; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

Oy		372	TCAATTATTTAGTATTTTAACTAATGTAATGTAATGTAATTTAACTAGC	433
Dd		22	TCAGCTATTAACGTATTTTAAATTAGTTAAATGTAATGTAATTTGTTACTAGC	81
Oy		432	TTTTTTTACTAGCAATTTTTTAGCCAACTAACATTAAGTTAGTGATTCGAATAATGCC	491
Dd		82	TAAATTCACCTAACAA-TTTTWAGNCAACTAATTAAGTTCTAATATACATTCAAACACCCC	140
Oy		492 T 492		
Dd		141 T 141		
<hr/>				
RESULT 7				
AAAS1324	ID	AAAS1324	standard; DNA; 13868 BP.	
XX		AAAS1324;		
XX	AC	26-SEP-2000	(first entry)	
DT		Z. mays MADS-box protein ZMM14 gene regulatory sequence.		
DE		ZMM14; maize; MIRK-type; MADS-box; DNA-binding; upper floret; spikelet;		
KM		inflorescence; grass; chromosome 1; monocotyledon; regulatory region;		
KW		disease resistance; flowering; growth regulator; herbicide; OSMADSL; ds.		
XX				
OS		Zea mays.		
XX		WO200037488-A2.		
PN		29-JUN-2000.		
XX		20-DEC-1999;	99WO-EP010116.	
PP		21-DEC-1998:	98EP-00124335.	
PR		29-OCT-1999;	99EP-00121591.	
PA		(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.		
XX		Cacharron J, Theissen G, Delau W, Saedler H;		
PI		WPI; 2000-452177/39.		
DR				
XX				
PT		Novel nucleic acids encoding proteins with the activity of proteins		
PT		expressed in the upper florets of spikelets of grass inflorescences		
PT		useful for producing plants with altered proteins levels or compositions.		
XX				
PS		Disclosure; Page 88-91; 93pp; English.		
XX				
CC		This is a regulatory region sequence from the maize (Zea mays) ZMM14 gene		
CC		which encodes a MIRK-type MADS-box protein. The protein is involved in		
CC		DNA-binding and is expressed in the upper florets of spikelets of grass		
CC		inflorescences. The ZMM8 and ZMM14 genes (see AAAS1322-23) map to		
CC		chromosomes 1 and 9, respectively, and are similar to OSMADSL from rice		
CC		(Oryza sativa). The ZMM8 and ZMM14 genes are useful for study of MADS-box		
CC		proteins in monocotyledons. The sequences can be used to produce		
CC		transgenic plants having altered level or composition of protein(s) in		
CC		the florets of spikelets, for modulating the number of kernels, for		
CC		conferring or improving disease resistance, generating late or early		
CC		flowering, expressing heterologous proteins in the upper florets in the		
CC		spikelets of grass inflorescences, modifying solute partition in florets,		
CC		improving kernel derived products, or the expression of enzymes affecting		
CC		any agronomic aspect of the kernel or the whole inflorescence. Compounds		
CC		identified as being activators or inhibitors of genes specifically		
CC		expressed in the spikelets of grass inflorescence may be used as growth		
CC		regulators and/or herbicides		
XX				
SQ		Sequence 13868 BP; 4120 A; 2725 C; 2718 G; 4305 T; 0 U; 0 Other;		
Query Match		5.0%; Score 62.6; DB 3; Length 13868;		
Best Local Similarity		56.7%; Pred. NO. 7.Se-03;		
Matches 160;		Conservative 0; Mismatches 111; Indels 11; Gaps 2		

PS Claim 1; SEQ ID NO 148; 27bp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 0 U; 8 Other;
SQ
Query Match 4.7%; Score 58; DB 4; Length 5689;
Best Local Similarity 49.5%; Pred. No. 0.00073;
Matches 145; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 187 TTGCTTTAAATCTAGACCACTGATTAATCTTTGACACAGATGTTATCTATTG 246
DB 1641 TTGTTTGGTTTATTAATGAATTAATATATTCGATTTTATTTGTTATTTTCG 1700
QY 247 TTGACTTTAATCAATCTAAATCCAGATTTAGTAGACATGTTACTATAGTAGCG 306
DB 1701 TTTTATTTTAAATTAATTAATTTTATTTTATTTTATTTTATTAATTAATTTT 1760
QY 307 AGTTTGAATGACAGCTAATAGTTAGTAAATTTAGTGAGACATTCACAA 366
DB 1761 TTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTAAATTTTAA 1820
QY 367 CCTATCAATTAATTTAGTTATTTTAAATTAATTTAGTTAGTTATTTTAAAG 426
DB 1821 ATTATTTTAAATTAATTAATTAATTAATTTTAAATTAATTTTATTTTATTT 1880
QY 427 CTAGCTTTTAACTAGCAATTTTAAAGCACTAACAATTTAGTTAGTGA 479
DB 1881 TATATTTTAAATTAATTAATTTTATTTTATTTTATTTTATTTTAAATTA 1933
RESULT 10
ABK28226
ID ABK28226 standard; DNA; 5689 BP.
AC ABK28226;
XX
XX 23-APR-2002 (first entry)
XX
XX DNA transcription associated complementary genomic DNA #50.
DE
XX
XX DNA transcription associated complementary genomic DNA #50.
XX
XX DNA transcription associated complementary genomic DNA #50.
XX
XX PNA: cytosine methylation state; SNP; retroviral infection; gene; ds;
XX single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
XX viral infection; Sezary syndrome; haematological disorder; tuberculosis;
XX immunological disorder; Werner syndrome; developmental disorder;
XX psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
XX neurodegenerative disorder; Maardenburg syndrome; Niemann-Pick disease;
XX myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
XX angiogenesis; congenital heart disease; HDR syndrome; gene therapy;

KM polyglutamine disorder; solid tumour.
XX
XX Unidentified.
XX
XX WO200192565-A2.
XX
XX
XX 06-DEC-2001.
XX
XX
XX 06-APR-2001; 2001WO-EP0039973.
XX
XX
XX 06-APR-2000; 2000DE-01019058.
XX
XX 07-APR-2000; 2000DE-01019173.
XX 30-JUN-2000; 2000DE-01032529.
XX 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX MPI; 2002-090046/12.
DR
XX
XX
XX New nucleic acids or oligomers, useful for diagnosing or treating
PT diseases associated with DNA transcription, e.g. immunological disorders,
PT Werner syndrome, psoriasis, myocardial infarction, solid tumors or
PT cancer.
XX
XX
XX
PS Claim 1; SEQ ID NO 100; 32bp; English.
XX
XX
XX The invention relates to a nucleic acid, which comprises a segment of the
CC chemically pretreated DNA of genes associated with DNA transcription from
CC one of 346 sequences, and an oligomer, in particular an oligonucleotide
CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
CC to the chemically pretreated DNA of genes associated with DNA
CC transcription. The set of oligomer probes are useful for detecting the
CC cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
CC in a chemically pretreated genomic DNA. The nucleic acids are useful for
CC diagnosing or treating diseases associated with DNA transcription
CC (particularly with the methylation status), e.g. adenosine deaminase
CC deficiency, viral infection, retroviral infection, Sezary syndrome,
CC haematological disorders, immunological disorders, Werner's syndrome,
CC tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,
CC neurological disorders, neurodegenerative disorders, Maardenburg
CC syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
CC infarction, hypertension, angiogenesis, erythropoiesis, congenital heart
CC disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours
CC or cancer. Sequences ABK28127-ABK28472 represent DNA transcription
CC associated genomic DNA molecules of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format directly from the European Patent
CC Office
XX
SQ Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 0 U; 8 Other;
Query Match 4.7%; Score 58; DB 6; Length 5689;
Best Local Similarity 49.5%; Pred. No. 0.00073;
Matches 145; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 187 TTGCTTTAAATCTAGACCACTGATTAATCTTTGACACAGATGTTATCTATTG 246
DB 1641 TTGTTTGGTTTATTAATGAATTAATATATTCGATTTTATTTGTTATTTTCG 1700
QY 247 TTGACTTTAATCAATCTAAATCCAGATTTAGTAGACATGTTACTATAGTAGCG 306
DB 1701 TTTTATTTTAAATTAATTAATTTTATTTTATTTTATTTTATTTTAAATTTT 1760
QY 307 AGTTTGAATGACAGCTAATAGTTAGTAAATTTAGTGAGACATTCACAA 366
DB 1761 TTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTAAATTTTAA 1820
QY 367 CCTATCAATTAATTTAGTTATTTTAAATTAATTTAGTTAGTTATTTTAAAG 426
DB 1821 ATTATTTTAAATTAATTAATTAATTAATTTTAAATTAATTTTATTTTATTT 1880

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
15-MAR-2001; 2001WO-EP002945.	4.5%; Score 56; DB 4; Length 10286;	209;	0;	255;	0;	0
15-MAR-2000; 2000DE-01013847.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
06-APR-2000; 2000DE-01019058.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
07-APR-2000; 2000DE-01019173.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
30-JUN-2000; 2000DE-01032529.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
01-SEP-2000; 2000DE-01043826.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
(EPIC-) EPIGENOMICS AG.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
Olek A, Plegenbrock C, Berlin K.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
WPI; 2001-602751/68.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
Designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
Claim 1; SEQ ID NO 14; 28bp; English.	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
Sequences AS45296-AS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylation in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0
Sequence 10286 BP; 2779 A; 298 C; 2326 G; 4883 T; 0 U; 0 Other;	45.0%; Pred. No. 0.0028;	209;	0;	255;	0;	0

DB	2684	ACNACGTAATAATACATCTTAATTAATTAATTAATTAAC	2641
RESULT 13			
ABK28148/c			
XX	ABK28148	standard; DNA; 10286 BP.	
XX	ABK28148;		
XX	23-APR-2002	(first entry)	
DE	DNA transcription associated complementary genomic DNA #11.		
XX			
KW	DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;		
KW	PNA; cytosine methylation state; SNP; retroviral infection; gene; ds;		
KW	single nucleotide polymorphism; adenosine deaminase deficiency; cancer;		
KW	viral infection; Sezary syndrome; haematological disorder; tuberculosis;		
KW	immunological disorder; Werner syndrome; developmental disorder;		
KW	psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;		
KW	neurodegenerative disorder; Maardenburg syndrome; Niemann-Pick disease;		
KW	myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;		
KW	angiogenesis; congenital heart disease; HDR syndrome; gene therapy;		
KW	polyglutamine disorder; solid tumour.		
XX			
OS	Unidentified.		
XX			
PN	WO200192565-A2.		
XX			
PD	06-DEC-2001.		
XX			
XX	06-APR-2001; 2001MO-EP003973.		
PF			
XX	06-APR-2000; 2000DE-01019058.		
PR	07-APR-2000; 2000DE-01019173.		
PR	30-JUN-2000; 2000DE-01032529.		
PR	01-SEP-2000; 2000DE-01043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Plegenbrock C, Berlin K;		
XX			
DR	WPI; 2002-090046/12.		
XX			
PT	New nucleic acids or oligomers, useful for diagnosing or treating		
PT	diseases associated with DNA transcription, e.g. immunological disorders,		
PT	Werner syndrome, psoriasis, myocardial infarction, solid tumors or		
PT	cancer.		
XX			
PS	Claim 1; SEQ ID NO 22; 32pp; English.		
XX			
CC	The invention relates to a nucleic acid, which comprises a segment of the		
CC	chemically pretreated DNA of genes associated with DNA transcription from		
CC	one of 346 sequences, and an oligomer, in particular an oligonucleotide		
CC	or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical		
CC	to the chemically pretreated DNA of genes associated with DNA		
CC	transcription. The set of oligomer probes are useful for detecting the		
CC	cytosine methylation state and/or single nucleotide polymorphisms (SNPs)		
CC	in a chemically pretreated genomic DNA. The nucleic acids are useful for		
CC	diagnosing or treating diseases associated with DNA transcription		
CC	(particularly with the methylation status), e.g. adenosine deaminase		
CC	deficiency, viral infection, retroviral infection, Sezary syndrome,		
CC	haematological disorders, immunological disorders, Werner syndrome,		
CC	tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,		
CC	neurological disorders, neurodegenerative disorders, Maardenburg		
CC	syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial		
CC	infarction, hypertension, angiogenesis, erythropoiesis, congenital heart		
CC	disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours		
CC	or cancer. Sequences ABK28127-ABK28472 represent DNA transcription		
CC	associated genomic DNA molecules of the invention. Note: The sequence		
CC	data for this patent did not form part of the printed specification but		
CC	was obtained in electronic format directly from the European Patent		
CC	Office		
XX			

PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-010834/01.

XX New nucleic acid, useful for diagnosis and therapy of metabolic disease,
PT solid tumor and cancers, comprises segment of chemically modified genomic
PT sequences of genes associated with metabolism.

PS Claim 1, Page 64-65; 143pp; English.

CC The invention relates to a nucleic acid (I) comprising a sequence at
CC least 18 bases of a segment of the chemically pretreated DNA of genes
CC associated with metabolism such as DUSP2 (NM_004418), EPHX2 (NM_001979),
CC QDPR (NM_000320), SCSH (NM_000199), SHMT2 (NM_005412), SLC7A2
CC (NM_003046), SLC7A4 (NM_004173) and TYMS (NM_001071) (all undefined). (I)
CC are useful for diagnosis and therapy of metabolic disease, solid tumours
CC and cancers; as primer oligonucleotides for the amplification of DNA
CC sequences, for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms (SNPs) in a chemically treated DNA of genes
CC associated with metabolism. An array of (I) is useful for ascertaining
CC genetic and/or epigenetic parameters for the diagnosis and/or therapy of
CC existing diseases or the predisposition to specific diseases by analysing
CC cytosine methylations. The method involves chemically treating genomic
CC DNA sample by a solution of bisulphite, hydrogen sulphite or disulphite
CC such that cytosine bases which are unmethylated at the 5th-position are
CC converted to uracil or another base which is dissimilar to cytosine in
CC terms of hybridisation behaviour and amplifying fragments of the
CC chemically pretreated genomic DNA. The genomic DNA is from cells or
CC cellular components which contain DNA, sources of DNA comprising, for
CC e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal
CC fluid, tissue embedded in paraffin such as tissue from eye, intestine,
CC kidney, brain, heart, prostate, lung, breast or liver, histologic object
CC slides and their combinations. Genetic parameters are mutations, in
CC particular insertions, deletions, point mutations, inversions and
CC polymorphisms of genes associated with metabolism and sequences further
CC required for their regulation. Epigenetic parameters are in particular
CC cytosine methylations and further chemical modifications of DNA bases of
CC genes associated with metabolism. Further epigenetic parameters include
CC for e.g. the acetylation of histones which correlates with DNA
CC methylation. AAS53306-AAS53373 represent chemically pretreated metabolism
CC associated genes, and related primers of the invention

XX SQ Sequence 6219 BP; 1714 A; 141 C; 1278 G; 3086 T; 0 U; 0 Other;

Query Match 4.4%; Score 55.2; DB 6; Length 6219;
Best Local Similarity 51.0%; Pred. No. 0.0037;

Matches 155; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

OY 150 TCAGACAGTGGTGAAGGTTTAACGACTAATATCTTGTCTTAATACTACCAAC 209
DB 2150 TTAGATTGTTGTTATTTGTTGTTGTTGTTTATTTAATGTTTGTGAAAGTTT 2209
OY 210 TGATTAATATCTTTCGACACATGTTAATATCTATGTTGACTTAATCAATACTAATC 269
DB 2210 TTATTAATATTTTATTAATTAAGGTTAAGAGTTAATTAATTAAGTATTAATTT 2269
OY 270 CAAGATATTAGTAGAGATTGATTAAGTTAAGTATGATGTTGAAATGCACTAGAGCTAA 329
DB 2270 AAAAATAAATGAAGAATAGTTAGTTTATTAAGGAAAGTTTATGAGAGGTGTGGAA 2329
OY 330 TAGTAGTAGTAAATTAATAGTTGAGACATTCACACACCTATCAATATTAGTATTTT 389
DB 2330 TTTATTTTGGTATTAGTAGGAGTGTGTTGTTGATGAAATTTGA-AATTAAATTTAATAAT 2388
OY 390 TAGTAATATTAGTTAATAGTTAGTTAGTTAATTAATAGTAGCTTTTCTTACTAGCAATTT 449
DB 2389 GGGGAAATTTTGAATTTGTGATTAGTATTTTGGGGTTATATGAGAGAGTTA 2448

OY 450 TTTA 453
DB 2449 TTTA 2452

Search completed: July 17, 2004, 12:35:12
Job time : 418 secs

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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 12:19:35 ; Search time 85 Seconds
(without alignments)
8141.456 Million cell updates/sec

Title: US-09-718-754A-1

Perfect score: 1247
Sequence: 1 atcgatcataaagttgacat.....agagtcgctagcaactagca 1247

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	102.6	8.2	4137	3 US-08-750-357-7	Sequence 7, Appl1
C 2	78.2	6.3	318	4 US-09-313-294A-7567	Sequence 7567, Ap
C 3	46.8	3.8	640681	4 US-09-790-988-1	Sequence 1, Appl1
C 4	45.8	3.7	8093	4 US-10-204-708-32	Sequence 32, Appl
C 5	44.6	3.6	20674	4 US-09-641-638-651	Sequence 651, App
C 6	44.4	3.6	5152	4 US-10-204-708-73	Sequence 73, Appl
C 7	44.2	3.5	6306	4 US-10-204-708-49	Sequence 49, Appl
C 8	43	3.4	6768	1 US-08-107-755A-1	Sequence 1, Appl1
C 9	43	3.4	8457	1 US-07-991-867B-1	Sequence 1, Appl1
C 10	43	3.4	8457	2 US-08-544-332-1	Sequence 1, Appl1
C 11	43	3.4	8457	4 US-09-370-861A-1	Sequence 1, Appl1
C 12	42.8	3.4	1664976	4 US-08-916-421B-1	Sequence 1, Appl1
C 13	42.6	3.4	7015	3 US-09-177-249-6	Sequence 6, Appl1
C 14	42	3.4	4539	1 US-08-119-512-1	Sequence 1, Appl1
C 15	42	3.4	4539	1 US-08-488-015B-1	Sequence 1, Appl1
C 16	42	3.4	4542	3 US-08-814-412-11	Sequence 11, Appl
C 17	41.4	3.3	1431	3 US-09-316-083-2	Sequence 2, Appl1
C 18	41.4	3.3	1431	4 US-09-333-700-2	Sequence 2, Appl1
C 19	41.4	3.3	5666	4 US-10-204-708-30	Sequence 30, Appl
C 20	41.2	3.3	20674	4 US-09-641-638-651	Sequence 651, App
C 21	41.2	3.3	58407	4 US-08-916-421B-2	Sequence 2, Appl1
C 22	41	3.3	19124	2 US-08-487-826B-13	Sequence 13, Appl
C 23	41	3.3	1664976	4 US-08-916-421B-1	Sequence 1, Appl1
C 24	40.8	3.3	1079	1 US-07-781-355-1	Sequence 1, Appl1
C 25	40.6	3.3	6317	4 US-10-204-708-11	Sequence 11, Appl
C 26	40.6	3.3	11049	4 US-10-204-708-21	Sequence 21, Appl
C 27	40.4	3.2	615	3 US-08-998-416-186	Sequence 186, App

28	40.4	3.2	636	3 US-08-998-416-1137	Sequence 1137, Ap
C 29	40.4	3.2	636	3 US-08-998-416-1137	Sequence 1137, Ap
C 30	40.4	3.2	837	3 US-08-998-416-288	Sequence 288, App
31	40.4	3.2	5152	4 US-10-204-708-74	Sequence 74, Appl
32	40	3.2	1609	3 US-09-377-648-1	Sequence 1, Appl1
33	40	3.2	6156	4 US-10-204-708-60	Sequence 60, Appl1
C 34	39.8	3.2	2334	1 US-08-062-632-4	Sequence 4, Appl1
C 35	39.6	3.2	6306	4 US-10-204-708-50	Sequence 50, Appl1
36	39.6	3.2	6583	4 US-10-204-708-26	Sequence 26, Appl
37	39.6	3.2	10640	4 US-09-417-485D-5	Sequence 5, Appl1
38	39.4	3.2	1887	4 US-09-601-198-39	Sequence 39, Appl
C 39	39.4	3.2	3095	6 US-09-790-988-1	Patent No. 5231168
C 40	39.4	3.2	640681	4 US-09-790-988-1	Sequence 1, Appl1
41	39.2	3.1	832	4 US-09-621-976-2813	Sequence 2813, Ap
C 42	39.2	3.1	11049	4 US-10-204-708-22	Sequence 22, Appl
C 43	39	3.1	19233	4 US-10-204-708-45	Sequence 45, Appl
C 44	38.8	3.1	828	3 US-08-998-416-538	Sequence 538, App
C 45	38.6	3.1	615	3 US-08-998-416-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-08-750-357-7/C
Sequence 7, Application US/08750357
Patent No. 6008437
GENERAL INFORMATION:
APPLICANT: KREBBERS, Enno
APPLICANT: WILLIAMS, Mark
APPLICANT: LEMANS, Jan
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,357
FILING DATE: 21-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 018030-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: E. coli-HindIII region of plasmid pCOL13
FEATURE:
NAME/KEY: prim_transcript
LOCATION: 188
NAME/KEY: exon
LOCATION: 188..212
FEATURE:

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NAME/KEY: intron
LOCATION: 213..556
FEATURE:
NAME/KEY: exon
LOCATION: 557..718
FEATURE:
NAME/KEY: intron
LOCATION: 719..1224
FEATURE:
NAME/KEY: exon
LOCATION: 1226..2771
OTHER INFORMATION: /codon start= 2
OTHER INFORMATION: /note="exon containing 3' end coding region of B-peru gene"
OTHER INFORMATION: This exon continues up to the polyadenylation site."
FEATURE:
NAME/KEY: CDS
LOCATION: 576..718
FEATURE:
NAME/KEY: CDS
LOCATION: 1226..2771
FEATURE:
NAME/KEY: -
LOCATION: 1269..2771
OTHER INFORMATION: /note= "fragment of B-peru coding
OTHER INFORMATION: region which is derived from cDNA"
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 2772..4137
FEATURE:
NAME/KEY: -
LOCATION: 1..6
OTHER INFORMATION: /label= EcoRI
FEATURE:
NAME/KEY: -
LOCATION: 11..16
OTHER INFORMATION: /label= XbaI
FEATURE:
NAME/KEY: -
LOCATION: 45..50
OTHER INFORMATION: /label= KpnI
FEATURE:
NAME/KEY: -
LOCATION: 265..270
OTHER INFORMATION: /label= HindIII
FEATURE:
NAME/KEY: -
LOCATION: 329..334
OTHER INFORMATION: /label= XbaI
FEATURE:
NAME/KEY: -
LOCATION: 835..840
OTHER INFORMATION: /label= BamHI
FEATURE:
NAME/KEY: -
LOCATION: 1269..1274
OTHER INFORMATION: /label= MluI
FEATURE:
NAME/KEY: -
LOCATION: 2788..2793
OTHER INFORMATION: /label= HindIII
FEATURE:
NAME/KEY: -
LOCATION: 2884..2889
OTHER INFORMATION: /label= MluI
FEATURE:
NAME/KEY: -
LOCATION: 2828..2833
OTHER INFORMATION: /label= HindIII
FEATURE:
NAME/KEY: -
LOCATION: 4114..4119
OTHER INFORMATION: /label= SalI
FEATURE:

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? NAME/KEY: -
? LOCATION: 4132..4137
? OTHER INFORMATION: /label= HindIII
? FEATURE:
? NAME/KEY: -
? LOCATION: 4114..4137
? OTHER INFORMATION: /label= polylinker
? OTHER INFORMATION: /note= "part of polylinker of pUC19"
? IS-08-750-357-7

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Query Match	8.2%;	Score 102.6;	DB 3;	Length 4137;
Best Local Similarity	72.2%;	Pred. No. 6.2e-18;		
Matches 151;	Conservative 0;	Mismatches 49;	Indels 9;	Gaps 1;

Qy 295 TGATTTAAGGTGATGTTTGAATCCACTAGAGCTAATAAGTTAGTAAATTAAGTTGGA 354

Db 3537 TTGCACTAAGGGGTGTTTGAATACACTAGAACCTAATAATGATCTCTAAATTAAGCTGAA 3478

Oy	355	GACATTCAACGCCCTA-----TCATTTATTAGTATTTTGTAGTAATTTGTAT	405
Db	3477	GACATCAACACATATAGCTAATTAATTCAGCTATTAGCTACTTTTGACCAATTAGCTAAT	3418

Db

OY 406 AGTGTAGTGTATTATTAAGCTGAGCTTTTTHACAGCAATTTTTHAGCCAAIACAA 463

3417 ATTAGCTAGCTATTATTAACCACTAATTTTAAATAGTAATTTTAAACCACTA 3358

Qy	466	TTAGTTTAGTGTATTCAATACCCCTTA	494
Db	3357	TTAGTTCAGTACATTTTAACACCTCTTA	3329

RESULT 2
US-09-313-294A-7567

Sequence 7567, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.

: APPLICANT: Ito, Laura Y.
 : APPLICANT: Sherman, Bradley K.
 : TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 : FILE REFERENCE: PL-0017 US
 : CURRENT APPLICATION NUMBER: IIS/09/713 294A

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:  
: CURRENT REFERENCE NUMBER: C070572172238  
:  
: CURRENT FILING DATE: 1999-05-14  
:  
: NUMBER OF SEQ ID NOS: 7600  
:  
: SOFTWARE: PERL Program  
:  
: SEQ ID NO 7567
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: LENGTH: 318
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: TYPE: DNA
:
: ORGANISM: Zea mays
:
: FEATURE:
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:

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: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. 6476212 70038194911
:
: NAME/KEY: unsure
: LOCATION: 101, 104, 234, 255, 258, 268, 280, 285-286, 289, 297, 314
: OTHER INFORMATION: a t c g or other

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Query Match	Score	DB	Length
Best Local Similarity	82.6%	Pred. No. 8,46-12	318

	Matches	100, Conservative	0, Mismatches	20, Indels	1, Gaps	1, ...
Oy	372	TCATTATTAGTATTTTGTAGTAATAGTAAATAGTACTTATTATAAGCTGAC	431			
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	99					
	98					
	97					
	96					
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	36					
	35		</			

D6	22	TCACGCTATGAGCTATTTTGGGAAATAGTTAAATAGTTAGGTAACCAATATGTTAGGCTACG	81
D5	432	TTTTTTTACGACATTTTTCAGCCACTAACAATTAGTTTACGTGTTAAATATACCC	491
QY	82	TAAATCCAGCAACA-TTTTATGACACTACATTTGTTCTAATATCAATCAACCC	140

Oy	492 T 492
	141 T 141
Nb	

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RESULT 3
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match      3.8%; Score 46.8; DB 4; Length 640681;
Best Local Similarity 47.1%; Pred. No. 0.071;
Matches 144; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 163 ATAGGTTAACTGATCTAATATCTTGTCTTAAATAGTACCACTGATATAATCTT 222
DB 268417 AAATATTAACAATAATATGATCTTTATTTTAAAAAATATCATCTTTATGTAAT 268358

QY 223 TCGAACACATGTTATATCTATTTGTTGACTTAAATCAATCAATCCAGATATTAGTA 282
DB 268357 TGAATAATCTATATATATATATTTTGGATATATATTAATCACTTAAATTAATTAAGAA 268298

QY 283 GAGATGTAGTATGATTAAGTGAATGTTGAATGACATAGAGCTAATAGTAGTACTA 342
DB 268297 AAGATCTTATCTATATATGTAATTAATTTACTATAGCAAAAAAATTTTAAACATA 268238

QY 343 AAATAGTTGAGACATTCMAACACCCCTATCAATATTAGTATTTTAAATTAAGTT 402
DB 268237 CAATCTATTTTAAATTAATAAATTTTATTTTGAAGTTTAAAGATGCTTACAGTAC 268178

QY 403 AATAGTATGTTAGTATTTATATAGCTAGCTTTTATTTACTAGCAATTTTACCAACTAA 462
DB 268177 AATATTATTTATCAACTTCMAAGACATCCCTAGACGCAAAAAATTTATGTCATCAAC 268118

QY 463 CAATTA 468
DB 268117 TAATGA 268112

RESULT 4
US-10-204-708-32
; Sequence 32, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PISENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 32
; LENGTH: 8093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-32

Query Match      3.7%; Score 45.8; DB 4; Length 8093;
Best Local Similarity 48.1%; Pred. No. 0.02;
Matches 163; Conservative 0; Mismatches 172; Indels 4; Gaps 1;

QY 214 AATAATCTTTGACACATGTTATTTATCTATTTGACTTTAATCAATCAATTCAG 273
DB 1834 ATTAATTAAGTATTAAGTATGATGTTTGTGTTTATAGTATTTGATAGT 1893

QY 274 ATATTAGTAGACATGTTAGTATAGATTAAAGTGATGTTGAATGACTAGACTAATGT 333
DB 1894 AATAATTAAGTGTGTTGTTGTTTAA- - -TTTATTTTAAATAGTAGAATAATAAGT 1949

QY 334 TAGTAGCTAAATTAAGTTGAGACATTCMAACACCCCTATCAATTTAGTTATTTTAGT 393
DB 1950 TAGTTGTTATTTGTTTGTGTTATTTATTTATTAAGTGAAGAAAGAAATATTTAGT 2009

QY 394 AAATAGTTAATAGTATGTTATTTATTAATTAAGCTTTTATTTACTAGCAATTTTAA 453
DB 2010 TTTGTTTATTTTATTTATTTATTTTAAATTTTATTTTATTTTATTTTATTTTAA 2069

QY 454 GCCACTAACAATTTGTTTATGTTATTCATTAATACCCCTAAGCCCTAAGTACTCT 513
DB 2070 TTTATGTTTATTTTATTTTATTTTATTTTGAATGTTTATTTTATTAATAAATTTT 2129

QY 514 TCTAGATCTTAAACCTATGTCGAGACAACTTTTCATA 552
DB 2130 AGAAATTTATTTATTTTAAATTTGAAGTATTTTATTTTAA 2168

RESULT 5
US-09-641-638-651/c
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BI-ALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent .pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1123-..3123
; OTHER INFORMATION: 5' regulatory region
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NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5563
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
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LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
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NAME/KEY: misc_feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
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NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele

LOCATION: 2832
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NAME/KEY: allele
LOCATION: 2844
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NAME/KEY: allele
LOCATION: 2934
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NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
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LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
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LOCATION: 6019
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NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
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LOCATION: 6338
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LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
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OTHER INFORMATION: 10-347-165 : polymorphic base C or T
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OTHER INFORMATION: 10-347-203 : polymorphic base A or G
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LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
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OTHER INFORMATION: 10-347-271 : polymorphic base A or T
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LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777

FILE REFERENCE: 5013.1012

; PRIOR FILING DATE: 2000-04-07

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; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 49
; LENGTH: 6306
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-49

Query Match
Best Local Similarity 47.1%; Score 44.2; DB 4; Length 6306;
Matches 136; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 178 ACTAATATCTGCTTTAATACAGACCACTGATTAATCTTCGAACACATGTTAT 237
DB 2545 AATTAATATTTATTTAGTAACTGTTGATGTGTGATTAATTAATTAAGTTAGGA 2604
QY 238 TATCTATGCTGCTTTAATCAATTAATCAAGATTAATAGATGTTAGTATAG 297
DB 2605 AGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2664
QY 298 ATTAAGTGAATGTTGAATGACCTAGACCTAATAGTATAGCTAATTAATTAAT 357
DB 2665 GGGAGAGTAAATGTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 2724
QY 358 ATTCGAACCCCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 417
DB 2725 TGATAGCTTTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2784
QY 418 ATTATAGCTAGCTTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 466
DB 2785 TTTTGTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2833

RESULT 8
US-08-107-755A-1/c
; Sequence 1, Application US/08107755A
; Patent No. 5721352
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,755A
; FILING DATE: 19-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,658
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
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; REFERENCE/DOCKET NUMBER: UP114.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Amsacta moorei entomopoxvirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (65..1459)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1474..2151
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2239..2475)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2502..2987
; FEATURE:
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (6277..6768)
US-08-107-755A-1

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 6768;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;
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RESULT 9
US-07-991-867B-1/c
; Sequence 1, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
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APPLICANT: Gruidi, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI14.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
LOCATION: 1474..2151
FEATURE:
NAME/KEY: CDS
LOCATION: complement (2239..2475)
FEATURE:
NAME/KEY: CDS
LOCATION: 2502..2987
FEATURE:
NAME/KEY: CDS
LOCATION: 3080..6091
FEATURE:
NAME/KEY: CDS
LOCATION: complement (6277..6768)
US-07-991-867B-1
Query Match 3.4%; Score 43; DB 1; Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.12;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;

QY 145 AACCATCAGCAGTGGTGTAGCTTAAGTACTAATATCTTGTCTTAATACTAGCA 204
|||||
DB 2315 AACCATCTACTAGTGTGGGAGATAAAGCTTAAGATAAATTATACCTAATA 2256
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QY 205 CCAACTGATTAATATCTTTCGAACACATCTATATCTATCTTGTGACTTAATCAATACT 264

DB 2255 GCAAAAAAAAAAATAAGCTGTAAATATGATATTAATAATATGACATAACCAATATATTT 2196
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DB 2195 TTAATCATTTTATTAATAAATATGTAGATTAATTAATATATGATTTAAGACA 2136
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QY 325 GCTAATAGTATAGCTAATAATTAAGTTGGAGACATTCACCAACCCATCATTAATAGTT 384
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DB 2135 AAAAGTCTCTAGCTGATATTTAAAAATGATTTATAGAGTATATTTATCTAATAT 2076
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QY 385 ATTT--TTAGTAATATAGTAAATAGTATGATTAATTAATAGCTTTTCTTACTA 442
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DB 2075 CTCACATTAGTATATAGCAAAATTTATATATTAATTAATAGATATATTAATTT 2016
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QY 443 GCAATTTTTCAGCACTAATTAAGTTTGTGATTCAAATACCCCTAAGCCGTTAA 502
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QY 503 GTGATGCTCTTCTAGAACTTAACCGTATG 533
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DB 1957 GTGATCTATATCTAATACATCATATTTTG 1927
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RESULT 10
US-08-544-332-1/C
Sequence 1, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidi, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UFI14.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:

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SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
LOCATION: 1474..2151
FEATURE:
NAME/KEY: CDS
LOCATION: complement (2239..2475)
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NAME/KEY: CDS
LOCATION: 2502..2987
FEATURE:
NAME/KEY: CDS
LOCATION: 3080..6091
FEATURE:
NAME/KEY: CDS
LOCATION: complement (6277..6768)
US-08-544-332-1
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Query Match 3.4%; Score 43; DB 2; Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.12;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;
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QY 205 CCACTGATTAATATCTTTCGAACACATGTTATCTATGTTGACTTTAATCAAT 264
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QY 385 ATTT--TTAGTAATTAAGTTAATGTTAGTATGTTAATTAAGCTATTTTACTA 442
DB 2075 CTCACATTAAGTATTAATAGCAAAATTAATTAATTAATTAATTAATTAAT 2016
QY 443 GCAATTTTTCAGCACTAATTAATTTAGTATTAATTAATTAATTAATTAAT 502
DB 2015 ACGGGATTTTCCCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1958
QY 503 GTGATGCTCTTCTAGCAATCTTAACCGTATG 533
DB 1957 GTGATCTATATCTAATATACATCACTATTTTG 1927
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RESULT 11
US-09-370-861A-1/c
Sequence 1, Application US/09370861A
Patent No. 6410221
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UFI14.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: US 07/827,685
PRIOR FILING DATE: 1992-01-30
PRIOR APPLICATION NUMBER: US 07/657,584
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 8457
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
US-09-370-861A-1
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Query Match 3.4%; Score 43; DB 4; Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.12;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;
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DB 1957 GTGATCTATATCTAATATACATCACTATTTTG 1927
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RESULT 12
US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
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/ OTHER INFORMATION: /product= "E3 exon"
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/ LOCATION: 1290..1559
/ OTHER INFORMATION: /product= "E5 exon"
US-08-119-512-1

Query Match          3.4%; Score 42; DB 1; Length 4539;
Best Local Similarity 47.5%; Pred. No. 0.17;
Matches 155; Conservative 0; Mismatches 170; Indels 1; Gaps 1;

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QY 140 CTTGCAACCATCAGACAGAGTGTGATAGTATTAACGATACATATCTGCTTTAATAC 199
DB 1942 AGTTAGATATTTACGATTTATGATATAAACAGATTAACCTTAATATATATATTA 2001
QY 200 TAGCACCACTGATATATATCTTTCCAGACATGTTATATCTATGTTGACTTTAATCA 259
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RESULT 15
US-08-488-015B-1
/ Sequence 1, Application US/08488015B
/ Patent No. 5780272
/ GENERAL INFORMATION:
/ APPLICANT: Jarell, Kevin A.
/ TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
/ TITLE OF INVENTION: AND REAGENTS
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley, Hoag & Eliot
/ STREET: One Post Office Square
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII (text)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,015B
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Vincent, Matthew P.
/ REGISTRATION NUMBER: 36,709
/ REFERENCE/DOCKET NUMBER: HDV-008.02
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 832-1000
/ TELEFAX: (617) 832-7000
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4539 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: both
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/ MOLECULE TYPE: other nucleic acid
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 969..1259
/ OTHER INFORMATION: /product= "E3 exon"
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1290..1559
/ OTHER INFORMATION: /product= "E5 exon"
US-08-488-015B-1

Query Match          3.4%; Score 42; DB 1; Length 4539;
Best Local Similarity 47.5%; Pred. No. 0.17;
Matches 155; Conservative 0; Mismatches 170; Indels 1; Gaps 1;

QY 20 TATCAATATCCATTTCACATTAATGAAACCAATTAATTAATAAACTAAATAAACTT 79
DB 1822 TATCAATATATATTTATATATATATATATATATATATATATATATATATATAT 1881
QY 80 TTATCACCGTACAGAGAAAGAGAGCATCACTGCTATTAGTTTATGCACTTAAACACC 139
DB 1882 TGTATTTGGAAATGAGCATACGATTAATCATATTAACCATAGTAAATTAATTTGAGAGCTA 1941
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QY 200 TAGCACCACTGATATATATCTTTCCAGACATGTTATATCTTATATGTTGACTTTAATCA 259
DB 2002 TATATAAAATAATATATATAT-ACCATATATATATATATATATATATATATATTA 2060
QY 260 ATACTTAATCCAGATATATAGTAGAGATGTAGTATAGATTAAGTGAGTTGAATGCA 319
DB 2061 ATTAATAATTAATATATATATATATATATATATATATATATATATATATATAGAA 2120
QY 320 CTAGAGCTAATAGTAGTAAATA 345
DB 2121 ATTTCTTATATTTAGAGGGTAAAA 2146
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-718-754A-1
Perfect score: 1247
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Gapop 10.0 , Gapext 1.0
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications NA.*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	104.6	8.4	925	US-10-039-836A-3	Sequence 3, Appl 1
C 2	82.4	6.2	1144	US-10-425-114-13740	Sequence 13740, A
C 3	77.8	6.2	1838	US-10-425-114-2342	Sequence 2342, Ap
C 4	70.8	5.7	790	US-10-389-566-170	Sequence 170, App
C 5	69	5.5	716	US-10-425-114-17635	Sequence 17635, A
C 6	69	5.5	1125	US-10-425-114-1825	Sequence 1825, Ap
C 7	69	5.5	2646	US-10-425-114-20790	Sequence 20790, A
C 8	67	5.4	555	US-10-425-114-17711	Sequence 17711, A
C 9	58	4.7	5689	US-10-221-714A-148	Sequence 148, App
C 10	58	4.7	5689	US-10-239-676-90	Sequence 90, Appl
C 11	58	4.7	5689	US-10-240-453-100	Sequence 100, App
C 12	56.6	4.5	1144	US-10-425-114-13740	Sequence 13740, A
C 13	56	4.5	10286	US-10-239-676-14	Sequence 14, Appl
C 14	56	4.5	10286	US-10-240-453-22	Sequence 22, Appl

15	55.2	4.4	6219	13	US-10-240-454-19	Sequence 19, Appl
16	55.2	4.4	6219	15	US-10-311-455-839	Sequence 839, App
17	54	4.3	14987	15	US-10-311-455-604	Sequence 604, App
18	52.4	4.2	555	13	US-10-425-114-17711	Sequence 17711, A
19	50.2	4.0	12142	15	US-10-311-455-1646	Sequence 1646, Ap
20	50.2	4.0	14924	15	US-10-311-455-198	Sequence 198, App
21	50.2	4.0	14924	15	US-10-240-452-22	Sequence 22, Appl
22	50	4.0	15714	15	US-10-311-455-1145	Sequence 1145, Ap
23	50	4.0	158001	17	US-10-211-179-11	GENERAL INFORMATION
24	49.8	4.0	925	15	US-10-039-836A-3	Sequence 3, Appl
C 25	49.8	4.0	1556	13	US-10-425-114-3445	Sequence 3445, Ap
26	49.8	4.0	8576	15	US-10-311-455-2201	Sequence 2201, Ap
27	49.6	4.0	6641	15	US-10-311-455-287	Sequence 287, App
28	49.6	4.0	6641	15	US-10-240-452-35	Sequence 35, App
29	49.4	4.0	6464	15	US-10-311-455-487	Sequence 487, App
30	49.4	4.0	6585	13	US-10-221-613-142	Sequence 142, App
31	49.4	4.0	6585	15	US-10-311-455-806	Sequence 806, App
32	49.2	3.9	8305	15	US-10-311-455-1541	Sequence 1541, Ap
33	49.2	3.9	3673778	15	US-10-312-841-2	Sequence 2, Appl
C 34	48.6	3.9	3991	15	US-10-074-045-60	Sequence 60, Appl
35	48.6	3.9	14798	15	US-10-311-455-1006	Sequence 1006, Ap
C 36	48.6	3.9	34722	17	US-10-322-281-700	Sequence 700, App
37	48.4	3.9	6123	15	US-10-311-455-793	Sequence 793, App
38	48.4	3.9	26997	13	US-10-221-714A-473	Sequence 473, App
C 39	48.4	3.9	271990	15	US-10-195-144-87	Sequence 87, Appl
C 40	48.4	3.9	271990	16	US-10-345-072-87	Sequence 87, Appl
C 41	48.2	3.9	17674	15	US-10-311-455-1318	Sequence 1318, Ap
42	48	3.8	5520	15	US-10-311-455-1491	Sequence 1491, Ap
43	47.8	3.8	6160	15	US-10-311-455-1506	Sequence 1506, Ap
C 44	47.6	3.8	11422	15	US-10-311-455-191	Sequence 191, App
C 45	47.6	3.8	11422	17	US-10-257-166-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-10-039-836A-3/c
; Sequence 3, Application US/10039836A
; Publication No. US20030033632A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; APPLICANT: Simmons, Carl
; TITLE OF INVENTION: Maize Proteinase Inhibitor-Like
; FILE REFERENCE: Polynucleotides and Methods of Use
; CURRENT APPLICATION NUMBER: US/10/039,836A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/243,167
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0).....(0)
; OTHER INFORMATION: Protease Inhibitor-Like promoter
US-10-039-836A-3

Query Match 8.4%; Score 104.6; DB 15; Length 925;
Best Local Similarity 79.7%; Pred. No. 1.8e-14;
Matches 165; Conservative 0; Mismatches 29; Indels 13; Gaps 3;

295 TGATTAGGATGTTGTTGAATGCTAGAGCTATTAGTACTTAATAATTAGTTGA 354
|||||
465 TAGACTTATGCGATCTGTTGAATGCTAGAGCTATTAGTACTTAATAATTAGTT 407
|||||
355 GACATTCAACAGCCCTATC-----AATTATAGTATTATTAGTAATTAGTTGA 404
|||||
406 GACATTCAACAGCCCACTTAATAATTAGTATTAGTATTATTAGTATTAGTTGA 347
|||||

RESULT 5

US-10-425-114-17635/c

; Sequence 17635, Application US/10425114
; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 17635

; LENGTH: 716

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3070-005-F5_FLI

US-10-425-114-17635

Query Match 5.5%; Score 69; DB 13; Length 716;

Best Local Similarity 70.8%; Pred. No. 4.7e-06;

Matches 138; Conservative 0; Mismatches 45; Indels 12; Gaps 3;

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 17635

; LENGTH: 716

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3070-005-F5_FLI

US-10-425-114-1825/c

; Sequence 1825, Application US/10425114
; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 1825

; LENGTH: 1125

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700167871_FLI

US-10-425-114-1825

Query Match 5.5%; Score 69; DB 13; Length 1125;

Best Local Similarity 70.8%; Pred. No. 6e-06;

Matches 138; Conservative 0; Mismatches 45; Indels 12; Gaps 3;

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 17635

; LENGTH: 716

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3245-244-G2_FLI

US-10-425-114-20790/c

; Sequence 20790, Application US/10425114
; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 20790

; LENGTH: 2646

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3245-244-G2_FLI

US-10-425-114-20790

Query Match 5.5%; Score 69; DB 13; Length 2646;

Best Local Similarity 70.8%; Pred. No. 9.6e-06;

Matches 138; Conservative 0; Mismatches 45; Indels 12; Gaps 3;

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 20790

; LENGTH: 2646

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3245-244-G2_FLI

US-10-425-114-17711/c

; Sequence 17711, Application US/10425114
; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

```

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17711
LENGTH: 555
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3075-006-G10_FLI
US-10-425-114-17711

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Query Match	5.4%;	Score 67;	DB 13;	length 555;
Best Local Similarity	62.9%;	Pred. No. 1.2e-05;		
Matches 144; Conservative	0;	Mismatches 70;	Indels 15;	Gaps 2;

QY	302	AGGTAAAGTTGAATGACCTAGAGCAATAGTACTACTGTAATTAATTTAGTGGACACTTC	361
QY <td>531</td> <td>AGGAGAGCTTAGGCCACCTAGAGATTAATAGTTACTATGACATCTTAGACATCTTAAC</td> <td>472</td>	531	AGGAGAGCTTAGGCCACCTAGAGATTAATAGTTACTATGACATCTTAGACATCTTAAC	472
Db <td>362</td> <td>AAACACCCCTA-----TCAATTATAGTATATTTTGTAAATTAAGTAAAGTTAGTAGT</td> <td>416</td>	362	AAACACCCCTA-----TCAATTATAGTATATTTTGTAAATTAAGTAAAGTTAGTAGT	416
QY <td>471</td> <td>AGCTGACGTAATAGTTTACTATTAATCTATTTTGGCAAATTAGCTAATAGTTAGATAA</td> <td>412</td>	471	AGCTGACGTAATAGTTTACTATTAATCTATTTTGGCAAATTAGCTAATAGTTAGATAA	412
Db <td>417</td> <td>TATTTAATAGCTAGCTTTTCTTTTACTAGCAATTTTTCGCCAATPACATTAAGTTTAGT</td> <td>476</td>	417	TATTTAATAGCTAGCTTTTCTTTTACTAGCAATTTTTCGCCAATPACATTAAGTTTAGT	476
QY <td>411</td> <td>TATTTGTAGCTAGTAATTTCAAC-----TTACTCAACTAATCATTAAGCTTAGT</td> <td>362</td>	411	TATTTGTAGCTAGTAATTTCAAC-----TTACTCAACTAATCATTAAGCTTAGT	362
Db <td>477</td> <td>GTAATCAATATCCCTTAAGCCGTTAAGTAGATGCTCTTTCTGAATCTTA</td> <td>525</td>	477	GTAATCAATATCCCTTAAGCCGTTAAGTAGATGCTCTTTCTGAATCTTA	525
QY <td>361</td> <td>ACGTTCAAAACACCTTTAGTCTAATAGCTAGCTAACTATTTGTGTAGCTAA</td> <td>313</td>	361	ACGTTCAAAACACCTTTAGTCTAATAGCTAGCTAACTATTTGTGTAGCTAA	313
Db <td></td> <td></td> <td></td>			

RESULT 9
US-10-221-714A-148
Sequence 148, Application US/10221714A
Publication No. US20040048254A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPNBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
PRIORITY FILING DATE: 2003-01-21
PRIORITY APPLICATION NUMBER: PCT/EP01/02955
PRIORITY FILING DATE: 2001-03-15
PRIORITY APPLICATION NUMBER: DE 10013847.0
PRIORITY FILING DATE: 2000-03-15
PRIORITY APPLICATION NUMBER: DE 10019058.8
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: DE 10019173.8
PRIORITY FILING DATE: 2000-04-07
PRIORITY APPLICATION NUMBER: DE 10032529.7
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: DE 10043826.1
PRIORITY FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 148
LENGTH: 5689
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:

```

; NAME/KEY: unsure
; LOCATION: 1818, 1930..1931, 1934..1935, 1947..1948, 1966
; OTHER INFORMATION: n is a or g or c or t
US-10-221-714A-148

```

Query Match	4.7%;	Score 58;	DB 13;	Length 5689;
Best Local Similarity	49.5%;	Pred. No. 0.006;		
Matches 145;	Conservative	0;	Mismatches 148;	Indels 0;
				Gaps 0;

Qy	187	TTGCTTTAAATACAGACACCACGTAAATATCTTTCGACGACATGTTATTAACATATG	246
Db	1641	TTGTTTGGTTTAAATGAAATTAATATATGCGATTTTATTTGTTATTAATTTTCG	1700
Qy	247	TTGACTTTAAATCAATACTAAATCCAGATATTTAGATGTTAGATTAATAGATTAAAGGTG	306
Db	1701	TTTTTTTTTAAATTTTAAATATTTTATTTTATTTTATTTTATTTTAAATATTAATTT	1768
Qy	307	ATGTTTGAATCCACTAGAGCTAATAGTTAGAGCTAAATATAGTTGGACATTCACAACA	366
Db	1761	TTTATTTTAAATATTTTTLATATTAATTTTTTTATTTTATTTTAAATTTTAAATTTTAA	1820
Qy	367	CCCATCATATATATAGTTATTTTATAGTAAATATAGTAAATAGTATTAATTTATAAG	426
Db	1821	ATTATTTTATTTTAAATATATATATATATATATATTTTAAATATTTTATTTTATTT	1880
Qy	427	CTAGCTTTTTTACTAGCAATTTTTTATGCCACACTACCAATTAAGTTTAAAGTGA	479
Db	1881	TATATTTTTTATTAATAAATTTTTTTTATATATATATATATATTTTTTTTTTAAATTA	1933

RESULT 10

US-10-239-676-90
; Sequence 90, Application US/10239676

```

1  / GENERAL INFORMATION:
2  / APPLICANT: OLEK, Alexander
3  / APPLICANT: PIEPENBROCK, Christian
4  / APPLICANT: BERLIN, Kurt
5  / TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
6  / FILE REFERENCE: 5013.1003
7  / CURRENT APPLICATION NUMBER: US/10/239, 676
8  / CURRENT FILING DATE: 2002-09-24
9  / PRIOR APPLICATION NUMBER: PCT/EP01/03968
10 / DE 10019058.8
11 / DE 10019173.8
12 / DE 10032529.7
13 / DE 10043826.1
14 / PRIOR FILING DATE: 2001-04-06
15 / 2000-04-06
16 / 2000-04-07
17 / 2000-06-30
18 / 2000-09-01
19 / NUMBER OF SEQ ID NOS: 228
20 / SEQ ID NO 90
21 / LENGTH: 5669
22 / TYPE: DNA
23 / ORGANISM: Artificial Sequence
24 / FEATURE:
25 / OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
26 / FEATURE:
27 / NAME/KEY: unsure
28 / LOCATION: (1818, 1930..1931, 1934..1935, 1947..1948, 1966)
29 / US-10-239-676-90

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Query Match	4.7%	Score 58;	DB 15;	length 5689;
Best Local Similarity	49.5%;	Pred. No. 0.006;		
Matches 145;	Conservative 0;	Mismatches 148;	Indels 0;	Gaps 0;

Oy 187 TTGCTTTAACTAGCACCACATGTAATAATCTTTCGAACACATGTATTATCTATG 246
| | | | | | | | | | | | | |
Oy 1641 TTTGGTTGTTTAATTAATGATTAATAAATATGGGTAATTTTATTTGTAATATTTTTCG 1700
| | | | | | | | | | | | | |
Oy 247 TTGACTTTAATCAATCTAAATCCAGATATTAGTAGATGTTAGTATTAAGTAAAGTG 306

```

QY 427 CTAGCTTTTCTTACTAGCAATTTTCTTACCACCACTAATTAAGTTTACTGTA 479
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1981 TATATTTTCTTATTAATTAATTTTCTTATATATATTAATTTTCTTATNNNTA 1933

RESULT 12
US-10-425-114-13740/c
; Sequence 13740, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13740
; LENGTH: 1144
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-037-C9-C9_FLI
US-10-425-114-13740

Query Match 4.5%, Score 56.6; DB 13; Length 1144;
Best local Similarity 62.2%; Pred. No. 0.0054;
Matches 125; Conservative 0; Mismatches 69; Indels 7; Gaps 2;

QY 291 AGTATAGATTAGGTGATGTTTGAATGACCTAGACTAATAGTTAGTACCTAAATYACT 350
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 397 AGGATGTACTAAGGGGGGTTTGAAGGCACTAGACTAATATGTTAGTGAACAAAAATY 338

QY 351 TGGAGACATTCACACCCCTATCAATTAATTAAGTTATTTTGTAAATTAAGTTAATAGTTA 410
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 337 ACTAG---TGGAAATTAGCTAGCAACTATTAAGTTTGTCTAAAGTAGCTAATAGCTG 282

QY 411 GTTAGTATTATTAATAGCTAGCTTTTCTTACTAGCAATTTTGTGCAACTAACAATTAAGT 470
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 281 AACATTAGCTAGACTGTTTGAAGTCTTACGCTAATTTT---AGCGCTAATCTATTAGC 225

QY 471 TTTAGTGTATTCAATACCCC 491
      |||||  |||||  |||||  |||||
Db 224 TTTAGCGCATTCACAAACACAC 204

RESULT 13
US-10-239-676-14/c
; Sequence 14, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239.676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03568
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01

```

NUMBER OF SEQ ID NOS: 228
SEQ ID NO 14
LENGTH: 10286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-14

Query Match
Best Local Similarity 45.0%; Score 56; DB 15; Length 10286;
Matches 209; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 25 AATATCCATTTCACCTAATAGAAACCAATTATTTAAAAAACCCTTAATC 84
DB 3104 AATTTAAATATTCATTAATCTTAAAAACAAAAATTAAAAAACAACCTAAACCAAAAAC 3045
QY 85 ACCGTACGAGAGAGAGACATCACTGCTATTAGTTTATGCACTTTAAACACCCCTTCG 144
DB 3044 CAATATCCCTTAAAAAATAATTAATACCTTAAAAATATTCGATTAATAATTAATAAAAA 2985
QY 145 AACCATCAGACAGTGGTGTAGTATGATGATCTAATATCTGTCTTAATACCTAGCA 204
DB 2984 AAAAAATTAATTAATAATTTTATTTTATTTATTTAATTAATAATTAATCAATCCAAAA 2925
QY 205 CCAACTGATTAATATCTTTCGACACATGTTATTAATCTATGTTGACCTTAATCAATACT 264
DB 2924 CTAAACAAATTTAAACCAAAAAACATCTAATACCTATTTTAAATTAATTAACCTTCAT 2865
QY 265 AATCCAGATATTTAGTAGAGATGTTAGTAGATTAAGGATGTTGAATGCACTAGA 324
DB 2864 TAAAAAAATCGAATAAAAAATTTATTTATTAATTAACCAAAAAAATATTAATCTAAA 2805
QY 325 GCTAATAGTATAGTAAATTAAGTTGAGACATTCACCAACCCATCAATTAATAGT 384
DB 2804 TCTATTAATAAAAAAACAATAAAATTTAAATTAATTTATTTCCCAAT 2745
QY 385 ATTTTATAGTAATTTAGTAAATTAAGTATTAATTAATTAAGCTTTTATTAAGC 444
DB 2744 AAAACTTAAAAAAATTTAATTTTATTTAGCATTTCAACATTCAGCTTTCAATATA 2685
QY 445 AATTTTTCGCACTAACATTAAGTTTATGCTATTCAAATAC 488
DB 2684 ACTAAGTAATTAACATTAATTAATTAATTAATTAATTAAC 2641

RESULT 14
US-10-240-453-22/C
Sequence 22, Application US/10240453
Publication No. US20030148326A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
FILE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350

LENGTH: 10286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-22

Query Match
Best Local Similarity 45.0%; Score 56; DB 15; Length 10286;
Matches 209; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 25 AATATCCATTTCACCTAATAGAAACCAATTATTTAAAAAACCCTTAATC 84
DB 3104 AATTTAAATATTCATTAATCTTAAAAACAAAAATTAAAAAACAACCTAAACCAAAAAC 3045
QY 85 ACCGTACGAGAGAGAGACATCACTGCTATTAGTTTATGCACTTTAAACACCCCTTCG 144
DB 3044 CAATATCCCTTAAAAAATAATTAATACCTTAAAAATATTCGATTAATAATTAATAAAAA 2985
QY 145 AACCATCAGACAGTGGTGTAGTATGATGATCTAATATCTGTCTTAATACCTAGCA 204
DB 2984 AAAAAATTAATTAATAATTTTATTTTATTTATTTAATTAATAATTAATCAATCCAAAA 2925
QY 205 CCAACTGATTAATATCTTTCGACACATGTTATTAATCTATGTTGACCTTAATCAATACT 264
DB 2924 CTAAACAAATTTAAACCAAAAAACATCTAATACCTATTTTAAATTAATTAACCTTCAT 2865
QY 265 AATCCAGATATTTAGTAGAGATGTTAGTAGATTAAGGATGTTGAATGCACTAGA 324
DB 2864 TAAAAAAATCGAATAAAAAATTTATTTAATTAACAAAAAATAATTTAATTTCTAAA 2805
QY 325 GCTAATAGTATAGTAAATTAAGTTGAGACATTCACCAACCCATCAATTAATAGT 384
DB 2804 TCTATTAATAAAAAAACAATAAAATTTAAATTAATTTATTTCCCAAT 2745
QY 385 ATTTTATAGTAATTTAGTAAATTAAGTATTAATTAATTAAGCTTTTATTAAGC 444
DB 2744 AAAACTTAAAAAAATTTAATTTTATTTAGCATTTCAACATTCAGCTTTCAATATA 2685
QY 445 AATTTTTCGCACTAACATTAAGTTTATGCTATTCAAATAC 488
DB 2684 ACTAAGTAATTAACATTAATTAATTAATTAATTAATTAATTAAC 2641

RESULT 15
US-10-240-454-19
Sequence 19, Application US/10240454
Publication No. US20040067491A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
FILE REFERENCE: 5013.1010
CURRENT APPLICATION NUMBER: US/10/240,454
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/04016
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 19

LENGTH: 6219
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-240-454-19

Query Match 4.4%; Score 55.2; DB 13; Length 6219;

Best Local Similarity 51.0%; Pred. No. 0.029;

Matches 155; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

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QY 150 TCAGCAGTGGTTGATAGGTTTAACTGATCTATATATCTGTCTTATATAGTACCAAC 209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2150 TTAGATTGTTGTTATTTGGTTGGTTGTTGTTTATATTTAATAGTTTGTGAAAGTTT 2209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 210 TCATATATATCTTTCACACATGTTATATCTATTTGTTGACTTATATCATATCTAATC 269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2210 TTATATATATTTTATATTAAGTTAAGTTAAGTTAATATTAAGTAAGTATTAATTT 2269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 270 CAAGATATTAGTAGAGATGTTAGTATAGATTAAAGTGATGTTGAATGCACTAGAGCTAA 329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2270 AAAAAATAAATGAAGATTAAGTTTATTTTGAAGAAAGTTTAAATGAGGTGTTGAA 2329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 330 TAGTAGTAGCTAAATAGTTGAGACATTCAAACACCTATCAATTATTAAGTTATTTT 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2330 TTTATTTTGGTATTAAGTGGGTTGTTGTTGTAAGAAATTGA-AATTATTTATTAATTT 2388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 390 TAGTAATATAGTTAATAGTTAGTTAGTTATTTAATAGCTAGCTTTTCTAGCAATTT 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2389 GGGGAAATTTGAATTGTTAGTTAGTTAGTTTATAGGGTTTATATGTAGAAAGTTA 2448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 450 TTTA 453
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DB 2449 TTTA 2452
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Search completed: July 17, 2004, 14:23:51

Job time : 458 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 12:17:49 ; Search time 2465 Seconds
(without alignments)
15106.750 Million cell updates/sec

Title: US-09-718-754A-1
Perfect score: 1247
Sequence: 1 atccgacataaagttgacat.....agagtcgctgacactagca 1247

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_escba:*
2: em_escbm:*
3: em_escin:*
4: em_escmu:*
5: em_escov:*
6: em_escpl:*
7: em_escro:*
8: em_escr:*
9: gb_esc1:*
10: gb_esc2:*
11: gb_esc3:*
12: gb_esc4:*
13: gb_esc5:*
14: gb_esc6:*
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16: em_escbm:*
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28: em_escpl:*
29: gb_esc1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	665.2	53.3	877	28	BZ791704 PUGBR37TD
2	614.2	49.3	933	28	BZ791700 PUGBR37TB
3	590.2	47.3	912	29	CG178223 PUFOS05TD
4	399	32.0	871	29	CG176077 PUBBP90TD

C 5	290	23.3	849	29	CG178220	CG178220 PUFOS05TB
6	251.4	20.2	647	29	CG678977	CG678977 OGJAI29TV
7	201.8	16.2	860	29	CG155338	CG155338 PUBH26TB
C 8	193	15.5	861	29	CG037363	CG037363 PUBH59TD
C 9	191.4	15.3	884	29	CG098858	CG098858 PUF2026TD
C 10	191.4	15.3	884	29	CG455835	CG455835 PUKG07TD
C 11	191.4	15.3	889	28	BZ795791	BZ795791 PUFQM22TB
C 12	191.4	15.3	891	28	BZ795799	BZ795799 PUFQM22TB
C 13	187.6	15.3	856	28	BZ786431	BZ786431 PUGBR92TB
C 14	187.4	15.0	844	28	CC014365	CC014365 PUBH07TD
C 15	187.4	15.0	905	29	CG132370	CG132370 PUGH42TB
C 16	185	14.8	791	28	CC013848	CC013848 PUBH94TD
C 17	173.8	13.9	852	28	CC007983	CC007983 PUDFV11TD
C 18	166.6	13.4	805	28	BZ825667	BZ825667 PUGFP95TB
C 19	157	12.6	696	29	CG043582	CG043582 PUBA11TD
C 20	156.4	12.5	756	29	CG236449	CG236449 OGZAA02TH
C 21	155.6	12.5	933	29	CG330662	CG330662 OG3CN08TV
C 22	151	12.1	692	28	BZ547228	BZ547228 OGALM25TC
C 23	151	12.1	836	29	CG098889	CG098889 PUFEX22TB
C 24	147.2	11.8	730	29	CG005872	CG005872 ZUAR457TV
C 25	147.2	11.8	803	29	CG277254	CG277254 OGXF15TV
C 26	146.2	11.7	666	29	CG853480	CG853480 ZMHB035
C 27	145.8	11.7	770	28	CG379956	CG379956 PUBH021TB
C 28	145.8	11.7	975	29	CG070123	CG070123 PUFPO06TD
C 29	143.8	11.5	811	28	CG373252	CG373252 PUFAC47TD
C 30	143.2	11.5	871	28	BZ679873	BZ679873 PUBH93TD
C 31	141.8	11.4	708	28	BZ525504	BZ525504 OGAGA49TC
C 32	141.8	11.4	786	28	CC017207	CC017207 PUBCD87TD
C 33	136.6	11.0	913	28	CG379954	CG379954 PUBH021TB
C 34	134.2	10.8	620	28	BZ622271	BZ622271 1977d04.9
C 35	133.8	10.7	714	28	BZ802691	BZ802691 PUFBE30TB
C 36	133.8	10.7	770	28	BZ535488	BZ535488 OGAGH65TC
C 37	133.2	10.7	313	28	BZ686702	BZ686702 PUBJ785TD
C 38	133.2	10.7	815	28	BZ703676	BZ703676 PUFCCU32TD
C 39	133.2	10.7	867	29	CG168508	CG168508 PUFPI42TB
C 40	133.2	10.7	917	29	CG441781	CG441781 OGVMH78TV
C 41	133	10.7	440	29	CG642979	CG642979 OGUCN86TV
C 42	133	10.7	862	29	CG157331	CG157331 PUFYH44TD
C 43	132.6	10.6	862	28	CC014963	CC014963 PUDAI18TD
C 44	132.2	10.6	755	28	BZ541495	BZ541495 OGAGB11TC
C 45	131.4	10.5	263	29	CG034521	CG034521 PUFSP95TD

ALIGNMENTS

RESULT 1
LOCUS BZ791704 877 bp DNA linear GSS 17-MAR-2003
DEFINITION PUGBR37TD ZM.0.6.1.0_KB Zea mays genomic clone ZMMBTA331H02,
genomic survey sequence.
ACCESSION BZ791704
VERSION BZ791704.1 GI:28988373
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 877)
AUTHORS Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and
Bennetzen, J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUGBR37TB
Contact: Cathy Whitehead
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehead@cigr.org
Seq primer: TF

FEATURES
source
Class: sheared ends.
Location/Qualifiers
1. 877
/organism="Zea mays"
/mol_type="genomic DNA"
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ORIGIN

Query Match 53.3%; Score 665.2; DB 28; Length 877;
Best Local Similarity 99.6%; Pred. No. 1.5e-127;
Matches 667; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 578 TGAATTAATATTTTACATGCGGTTCTTTAGCAAAACCGCACTGCTAATGATTTAG 637
DB 8 TGATATATATATTTTACATGCGGTTCTTTAGCAAAACCGCACTGCTAATGATTTAG 67
QY 638 ACTAGCGGCGTGTCTAAGAAACCGCGCTAAAGATTTTACCTAGCGGTTGTCTA 697
DB 68 ACTAGCGGCGTGTCTAAGAAACCGCGCTAAGATTTTACCTAGCGGTTGTCTA 127
QY 698 ACAACTGCTGTGAAAAAGCGATTCCTACTAGCCCTAGCTGCACTGCGACATAA 757
DB 128 ACAACTGCTGTGAAAAAGCGATTCCTACTAGCCCTAGCTGCACTGCGACATAA 187
QY 758 AAACGTGCTGAAATAGCTTCTAGATGCTCACTATAGAGCTTCTATGTTAGTGT 817
DB 188 AAACGTGCTGAAATAGCTTCTAGATGCTCACTATAGAGCTTCTATGTTAGTGT 247
QY 818 AGAAGTATGTTAGTGTGCAAGCAAGTGTCTTAAACCAATTAATTAATTAATTA 877
DB 248 AGAAGTATGTTAGTGTGCAAGCAAGTGTCTTAAACCAATTAATTAATTAATTA 307
QY 878 AATATATATGATGCTGAATTCGATTTCTATAGTAATGTTGCTTGCAACCGCAAT 937
DB 308 AATATATATGATGCTGAATTCGATTTCTATAGTAATGTTGCTTGCAACCGCAAT 367
QY 938 AAGATTAACATGCTGTCTGACAGAAATCCACATTAATAGAGTCCATGCGCGCGCA 997
DB 368 AAGATTAACATGCTGTCTGACAGAAATCCACATTAATAGAGTCCATGCGCGCGCA 427
QY 998 CGTACCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGCACTTTGCCGA 1057
DB 428 CGTACCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGCACTTTGCCGA 487
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DB 488 TCAGACAGTGTGACAGACCGGACCAATAGAAAGAAAGACAGACGCGCGGACCGCG 547
QY 1118 AGTAGGTGATGATCGTCAAGTTCGATTTTTCAGAGCGTGTCTGTAAATACGTAG 1177
DB 548 AGTAGGTGATGATCGTCAAGTTCGATTTTTCAGAGCGTGTCTGTAAATACGTAG 607
QY 1178 CCGTTTCACAAAGCGAGGCAAGGGGGAGAGATATGCTAGCTAGAGAGAGTGCCTA 1237
DB 608 CCGTTTCACAAAGCGAGGCAAGGGGGAGAGATATGCTAGCTAGAGAGAGTGCCTA 667
QY 1238 GCAACTAGCA 1247
DB 668 GCAACTAGCA 677

RESULT 2
BZ791700/c 933 bp DNA linear GSS 17-MAR-2003
LOCUS BZ791700
DEFINITION PUGBR37TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMBR331H02,
genomic survey sequence.
ACCESSION BZ791700
VERSION BZ791700.1 GI:28988365

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 933)
Whiteley,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Bennett,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,D. and
Bennett,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUGBR37TD
Contact: Cathy Whiteley
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1. 933
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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COT selected genomic DNA library"

ORIGIN

Query Match 49.3%; Score 614.2; DB 28; Length 933;
Best Local Similarity 99.5%; Pred. No. 5.5e-117;
Matches 616; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 629 GATATTTACACTAGCGGCGTCTAAGAAACCGCGCTGCTAAAGATTTTACACTAGC 688
DB 933 GATATTTACACTAGCGGCGTCTAAGAAACCGCGCTGCTAAAGATTTTACACTAGC 874
QY 669 GGTGTGAACAACCTGCTGTGAAAAAGCGATTCCTACTAGCCCTAGCTTGACCTG 748
DB 873 GGTGTGAACAACCTGCTGTGAAAAAGCGATTCCTACTAGCCCTAGCTTGACCTG 814
QY 749 CGACATAAAAAAGCTGTAAGAAATAGCTAGATGCTCACTATAGAGCTTCTATGTA 808
DB 813 CGACATAAAAAAGCTGTAAGAAATAGCTAGATGCTCACTATAGAGCTTCTATGTA 754
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QY 869 AATACTAGTAATATATATAGTGTGTAATTCGATTTCTATAGTAATGTTGCTTGCAA 928
DB 693 AATACTAGTAATATATATAGTGTGTAATTCGATTTCTATAGTAATGTTGCTTGCAA 634
QY 929 GCGCAATTAAGATTAATATGTTGCTGTGACAGAAATCCACTTACATTAAGTGCATGCG 988
DB 633 GCGCAATTAAGATTAATATGTTGCTGTGACAGAAATCCACTTACATTAAGTGCATGCG 574
QY 989 GCGCGGCGACGTAATCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGACA 1048
DB 573 GCGCGGCGACGTAATCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGACA 514
QY 1049 GTTGCGCATGACAGTGTGACAGACCGGACCAATAGAAAGAAAGACGACGCGCGCG 1108
DB 513 GTTGCGCATGACAGTGTGACAGACCGGACCAATAGAAAGAAAGACGACGCGCGCG 454
QY 1109 GCACCGCGAGTAGTGTGATGCTACGCTAGCTGATGCTTTTTCAGAGCGCTGCTGTA 1168
DB 453 GCACCGCGAGTAGTGTGATGCTACGCTAGCTGATGCTTTTTCAGAGCGCTGCTGTA 394

OY		1169	AATACGTGACCCCTTCACAAGCGAGGCAGAAGGGGGAGAGATATGTCAGCTAGCAGAGA	1228
Dδ		393	AATACGTGACCCCTTCCACAAGCGAGGCAGAAGGGGGAGAGATATGTCAGCTAGCAGAGA	334
OY		1229	GAGTGCGTAGCAACTAGCA	1247
Dδ		333	GAGTGCGTAGCAACTAGCA	315
RESULT 3				
CGI78223				
LOCUS				
DEFINITION	CGI78223	912 bp	DNA	linear GSS 21-AUG-2003
	PUDOS05TD ZM_0.6.1.0_KB	Zea mays	genomic clone ZMWBRa0711B09,	
ACCESSION	CGI78223			
VERSION	CGI78223.1	GI:34069284		
KEYWORDS	GSS.			
SOURCE	Zea mays			
ORGANISM	Zea mays			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 912)	Whitlaw, C.A., Quackenbush, J., Van Aken, S., Uetreback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.	Maize Genomics Consortium	Unpublished (2003)	Other GSSs: PUFQSO5TB

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TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitejaw@ctgr.org
Seq primer: TP
Class: sheared ends.

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FEATURES
:      source      Location/Qualifiers
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Cor selected genomic DNA library"

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ORIGIN

Query Match	47.3%	Score 590.2	DB 29	Length 912
Best Local Similarity	99.5%	Pred. No. 5.2e-112		
Matches 592	Conservative 0	Mismatches 3	Indels 0	Gaps 0

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Db	12	AAAAAACC	CGCCGCTCTAAAGATATTTACATACGCGTGGTGAAACAATCGCCGTGAA	71
Qy	713	AAAGCCGATTCCTACTAGCCCTAGCTTGCACTGCGACATMAAAAAAGTCAGTGAAAA	77.7	
Db	72	AAAGCCGATTCCTACTAGCCCTAGCTTGCACTGCGACATMAAAAAAGTCAGTGAAAA	133	
Qy	773	TACCTTAGAGATGTCACATAGAGCTTCTATGATCTTAGAGGTGAGAACATGATATGTA	83.2	
Db	132	TACCTTAGAGATGTCACATAGAGCTTCTATGATCTTAGAGGTGAGAACATGATATGTA	191	
Qy	833	GTGCACCAAGTGCAGATTTTAACTTAAACCAATACTAAATACATGATAAATACTAGTGG	89.2	
Db	192	GTGCACCAAGTGCAGATTTTAACTTAAACCAATACTAAATACATGATAAATACTAGTGG	251	
Qy	893	TCTGAATTCGATTTCTATAGTAATGTTTGCTTGCAAGCCGCAATATAGTAAACATTCGT	95.5	
Db	252	TCTGAATTCGATTTCTATAGTAATGTTTGCTTGCAAGCCGCAATATAGTAAACATTCGT	311	

QY	953	CGTCACGAAGATCCACATTTTCATCAAGATGCATGGCCGGCCACGATACCATCCACAG	1012
QY <td>312</td> <td>CGTCACGAAGATCCACATTTTCATCAAGATGCATGGCCGGCCACGATACCATCCACAG</td> <td>371</td>	312	CGTCACGAAGATCCACATTTTCATCAAGATGCATGGCCGGCCACGATACCATCCACAG	371
QY <td>1013</td> <td>CGTCGCTGCGAGGACACGTTGTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAG</td> <td>1072</td>	1013	CGTCGCTGCGAGGACACGTTGTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAG	1072
Db <td>372</td> <td>CGTCGCTGCGAGGACACGTTGTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAG</td> <td>431</td>	372	CGTCGCTGCGAGGACACGTTGTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAG	431
QY <td>1073</td> <td>ACCGGACAAATAGAAAGAAAGACGACGACGGCCGGCCACCGCCGAAATAGGTGATGTC</td> <td>1132</td>	1073	ACCGGACAAATAGAAAGAAAGACGACGACGGCCGGCCACCGCCGAAATAGGTGATGTC	1132
Db <td>432</td> <td>ACCGGACAAATAGAAAGAAAGACGACGACGGCCGGCCACCGCCGAAATAGGTGATGTC</td> <td>491</td>	432	ACCGGACAAATAGAAAGAAAGACGACGACGGCCGGCCACCGCCGAAATAGGTGATGTC	491
QY <td>1133</td> <td>ACGCTAGCTGTAGCTTTTTCAGAGCGTCGCTGTAAATACGTAGCCCTTCCACAAGGGA</td> <td>1192</td>	1133	ACGCTAGCTGTAGCTTTTTCAGAGCGTCGCTGTAAATACGTAGCCCTTCCACAAGGGA	1192
Db <td>492</td> <td>ACGCTAGCTGTAGCTTTTTCAGAGCGTCGCTGTAAATACGTAGCCCTTCCACAAGGGA</td> <td>551</td>	492	ACGCTAGCTGTAGCTTTTTCAGAGCGTCGCTGTAAATACGTAGCCCTTCCACAAGGGA	551
QY <td>1193</td> <td>GGCAAGGGGGGAGAGATATCGTACGTACGACAGAGAGTGCCTAGACATAGCA</td> <td>1247</td>	1193	GGCAAGGGGGGAGAGATATCGTACGTACGACAGAGAGTGCCTAGACATAGCA	1247
Db <td>552</td> <td>GGCAAGGGGGGAGAGATATCGTACGTACGACAGAGAGTGCCTAGACATAGCA</td> <td>606</td>	552	GGCAAGGGGGGAGAGATATCGTACGTACGACAGAGAGTGCCTAGACATAGCA	606

RESULT	4
LOCUS	CGI76077
DEFINITION	CGI76077 871 bp DNA linear GSS 21-AUG-2003 PUBB90TD ZM_0.6_1.0 KB Zea mays genomic clone ZMMBRA0631012,
ACCESSION	CGI76077
VERSION	CGI76077.1
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays

SOURCE	Zea mays
ORGANISM	Zea mays

REFERENCE
AUTHORS

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 871)

Whitelaw, C. A., Quackenbush, J. J., Van Aken, S., Uutterback, T., Resnick, A., Fraser, C. M., Yuan, Y., San Miguel, P., Ma, J. and

TITLE	Author
Bennetzen, J.	Maize Genomics Consortium

JOURNAL Unpublished (2003)
COMMENT Other GSSs: PU0BP90TB
Contact: Cathy Whitelaw
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9712 Medical Center Drive, Rockville, MD 20850, USA

JOURNAL
COMMENT
Unpublished (2003)
Other GSRS: PUBBP07B
Contact: Cathy WhiteLaw
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLaw@cigr.org

Seq primer: TF

```

FEATURES
    source
        location/Qualifiers
            1..871
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            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
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            /clone_1fb="ZM 0.6-1.0 kb"
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            Cor selected genomic DNA library"

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ORIGIN

Query Match	32.0%	Score 399	DB 29	Length 871
Best Local Similarity	100.0%	Pred. NO. 2e-72		
Matches 399	0	Mismatches 0	Indels 0	Gaps 0

QY	845	TTTTAATTAAACCAATACCTAAATATCTAGTGGTCGAATTCGATTTCT	908
Db	1	TTTTAATTAAACCAATACCTAAATATCTAGTGGTCGAATTCGATTTCT	60
QY	909	ATATGTAATGTTGCTTGCAAGCCGCAATAGATGAACATTGTCGTACAGAAATCCAC	968
Db	61	ATATGTAATGTTGCTTGCAAGCCGCAATAGATGAACATTGTCGTACAGAAATCCAC	120

QY 969 ATTACATCAAGGTCATGCGCGCGCCGACAGTACCCACGCGCTCGTCGCGAGAC 1028
|
|
|
Db 121 ATTACATCAAGGTCATGCGCGCGCCGACAGTACCCACGCGCTCGTCGCGAGAC 180
|
|
|
QY 1029 ACGTGTGGCTTACCGGACAGTTGGCCGATCAGACAGTGAACAGACCGGACATAGAGA 1088
|
|
|
Db 181 ACGTGTGGCTTACCGGACAGTTGGCCGATCAGACAGTGAACAGACCGGACATAGAGA 240
|
|
|
QY 1089 AGAAGACGACGACGCGGGGGGACCGCCGAGTAGAGTGCATGCTACGCTAGTACGTT 1148
|
|
|
Db 241 AGAAGACGACGACGCGGGGGGACCGCCGAGTAGAGTGCATGCTACGCTAGTACGTT 300
|
|
|
QY 1149 TTTCGAGACGCTCGTCTGTAATACGTAGCCCTTCCACAAGCGAGGCAAGGGGGAGAGA 1208
|
|
|
Db 301 TTTCGAGACGCTCGTCTGTAATACGTAGCCCTTCCACAAGCGAGGCAAGGGGGAGAGA 360
|
|
|
QY 1209 GTATGCTCAGCTACGACAGAGAGTGGTGTGCAACTTGCA 1247
|
|
|
Db 361 GTATGCTCAGCTACGACAGAGAGTGGTGTGCAACTTGCA 399
|
|
|

RESULT 5

CG178220/c 849 bp DNA linear GSS 21-AUG-2003
LOCUS PUFQ505TB.ZM.0.6.1.0.KB.Zea.mays.genomic.clone.ZM87A0711B09,
DEFINITION genomic survey sequence.
ACCESSION CG178220
VERSION CG178220.1 GI:34069281
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

1 (bases 1 to 849)
Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFQ505TB
COMMENT Contact: Cathy Whiteclaw

TITLE

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteclaw@tigr.org
Seq primer: TR
Classes: sheared ends.

FEATURES

Location/Qualifiers
1..849

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A0711B09"
/clone_1lb="ZM.0.6.1.0.KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN

Query Match 23.3%; Score 290; DB 29; Length 849;
Best Local Similarity 100.0%; Pred. No. 7.4e-50;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 CAGAAATCCATTCATCATCAAGTCCATGCGCGCGCCGACAGTACCCATCCACGCGTGC 1017
|
|
|
Db 849 CAGAAATCCATTCATCATCAAGTCCATGCGCGCGCCGACAGTACCCATCCACGCGTGC 790
|
|
|
QY 1018 CTGCGGAGGACACGCTTGGCTGACCGGACAGTTGGCCGATCAGACAGTGAACAGCCGG 1077
|
|
|
Db 789 CTGCGGAGGACACGCTTGGCTGACCGGACAGTTGGCCGATCAGACAGTGAACAGCCGG 730
|
|
|

QY 1078 ACAATAGAAGAAGAGACAGACCGCGCGGACCGCCGAGTAGAGTGCATGTCACGCT 1137
|
|
|
Db 729 ACAATAGAAGAAGAGAGAGACCGCGCGGACCGCCGAGTAGAGTGCATGTCACGCT 670
|
|
|
QY 1138 AGCTTAGCTTTTTCAGAGCGCTCGTGTAAATACGTAGCCCTTCCACAAGCGAGGCA 1197
|
|
|
Db 669 AGCTTAGCTTTTTCAGAGCGCTCGTGTAAATACGTAGCCCTTCCACAAGCGAGGCA 610
|
|
|
QY 1138 GGGGGGAGAGATATCGTACGTAGCAGAGAGAGTGCCTAGCACTAGCA 1247
|
|
|
Db 609 GGGGGGAGAGATATCGTACGTAGCAGAGAGAGTGCCTAGCACTAGCA 560
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|
|

RESULT 6

CC678977 647 bp DNA linear GSS 19-JUN-2003
LOCUS OGJA129TV.ZM.0.7.1.5.KB.Zea.mays.genomic.clone.ZM87A0294E09,
DEFINITION genomic survey sequence.
ACCESSION CC678977
VERSION CC678977.1 GI:32083753
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

1 (bases 1 to 647)
Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Kohling, T.,
Citek, R.W., Numborg, A., Robbins, D., and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
COMMENT Contact: Cathy Whiteclaw

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteclaw@tigr.org
Seq primer: TR
Classes: sheared ends.

FEATURES

Location/Qualifiers
1..647

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A0294E09"
/clone_1lb="ZM.0.7.1.5.KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 20.2%; Score 251.4; DB 29; Length 647;
Best Local Similarity 99.2%; Pred. No. 7.6e-42;
Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 993 CATGGCGGCGGCGGACGTAACCATCCACGCGCTGCTCGGAGGACAGTGTGGCTGAC 1042
|
|
|
Db 1 CATGGCGGCGGCGGACGTAACCATCCACGCGCTGCTCGGAGGAC-CTTGTGGCTGAC 59
|
|
|
QY 1043 CGGACAGTTGGCCGATCAGACAGTGAACAGACCGGACATAGAGAGAGAGAGAGAG 1102
|
|
|
Db 60 CGGACAGTTGGCCGATCAGACAGTGAACAGACCGGACATAGAGAGAGAGAGAGAGAG 119
|
|
|
QY 1103 GCGGCGGACCGGCGGAGTAGTGCATGTGTCACGCTGTAAGCTTTTTCAGAGCGTGC 1162
|
|
|
Db 120 GCGGCGGACCGGCGGAGTAGTGCATGTGTCACGCTGTAAGCTTTTTCAGAGCGTGC 179
|
|
|
QY 1163 TCTGTAAATAGGTAGCCCTTCCACAAGGAGGCAAGGGGGAGAGAGATGTCAGCTAG 1222
|
|
|
Db 180 TCTGTAAATAGGTAGCCCTTCCACAAGGAGGCAAGGGGGAGAGAGATGTCAGCTAG 239
|
|
|
QY 1223 CAGAGAGAGTGCGTAGCAACTAGCA 1247
|
|
|

|||||
Db 240 CAGAGAGAGTGGCTACCACTAGCA 264

RESULT 7
CG155338
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CG155338 860 bp DNA linear GSS 21-AUG-2003
PUIH26TB_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMMBTA0589F04,
CG155338
CG155338.1 GI:34046139
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 860)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUIH26TD
Contact: Cathy Whitelaw

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..860
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0589F04"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

FEATURES
source

16.2%; Score 201.8; DB 29; Length 860;
Best Local Similarity 84.2%; Pred. No. 1.3e-31;
Matches 240; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

Query Match
Best Local Similarity 84.2%; Pred. No. 1.3e-31;
Matches 240; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

525 AACCGATGTGGAGACAATTTTCATAGTGTAAGTCACTGATGATGATTAAT 584
|||||
107 AACCGATGTGGAGACAATTTTCATAGTGCGGGCTGCATMACACCGCATGATTAAT 166
|||||
585 AATATTTTCACATGCGGTTCTTAAGCAAAACCGCAGTGTATGATTTTACACTAGCG 644
|||||
167 AATATTTTCACATGCGGTTCTTAAGTAACTGCCAGTGTATGATTTTACACTAGCGG 226
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645 GGCTGCTAAAGAAACCGCCGCTAAAGATTTTACACTAGCGGTTGTGAACAATG 704
227 GGAGCTTAAGAAACGTCAGTGCTAATGATTTTACACTGCGGTTGGTAAACCA 286
|||||
705 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTTACGCTTGACATGCGACATAAAAACGTC 764
|||||
287 CCTGTGAAAAAAGCAATTTCTACTAGCCCTTACGAT--TGCGGCACACTGAAAAACGCC 343
|||||
765 AGTGAATAATAGCTCTAGATCGTCAATATGAGACTTCTATGACT 809
|||||
344 AGTGCAATAGCTCTAGAGCCGCACTATAGAGCTTCGTTACT 388

RESULT 8
CG037363/c
LOCUS
DEFINITION

CG037363 861 bp DNA linear GSS 19-AUG-2003
PUFNUS9TD_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMMBTA0690I22,

genomic survey sequence.
CG037363
CG037363.1 GI:33909519
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 861)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFNUS9TB
Contact: Cathy Whitelaw

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..861
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

FEATURES
source

15.5%; Score 193; DB 29; Length 861;
Best Local Similarity 84.6%; Pred. No. 8.9e-30;
Matches 241; Conservative 0; Mismatches 40; Indels 4; Gaps 2;

Query Match
Best Local Similarity 84.6%; Pred. No. 8.9e-30;
Matches 241; Conservative 0; Mismatches 40; Indels 4; Gaps 2;

525 AACCGATGTGGAGACAATTTTCATAGTGTAAGTCACTGATGATGATTAAT 584
|||||
606 AACCGATGTAGAGACAATTTTCATAGGCG-GCTGCTTAAGACACCGCCAGTATTAAT 548
|||||
585 AATATTTTCACATGCGGTTCTTAAGCAAAACCGCAGTGTATGATTTTACACTAGCG 644
|||||
547 AATATTTTCACATGCGGTTCTTAAGCAAAACCGCAGTGTATGATTTTACACTAGCG 488
|||||
645 GGCTGCTAAAGAAACCGCCGCTAAAGATTTTACACTAGCGGTTGTGAACAATG 704
487 GGCTGCTAAAGAAACCGCAGTGTATGATTTTACACTAGCGTTGACATTAACAACCG 428
|||||
705 CCTGTGAAAAAAGCGATTTCTACTAGCCCTTACGCTTGACATGCGACATAAAAACGTC 764
427 CCTGTGAAAAAAGCGCATTTCTACTAGCCCTTACGACACTGAC---GGCACTGAAAAATGCG 371
|||||
765 AGTGAATAATAGCTCTAGAGTGTCACTATAGAGCTTCTATGACT 809
370 AGTATTAATAGCTCTAGAGCCGACACTATAGAGCTTCTGTACT 326

RESULT 9
CG098858/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CG098858 872 bp DNA linear GSS 20-AUG-2003
PUFQ026TD_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMMBTA0769F03,
CG098858
CG098858.1 GI:33981152
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 872)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFQ26TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..872
Location/Qualifiers

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A0769F03"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 15.3%; Score 191.4; DB 29; Length 872;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGATGAGAGACAACATTTTCTAGAGTACTGTTTAAAGTACCGTCAGTATAT 584
DB 653 AACCGATGAGAGACAACATTTTCTAGAGTACTGTTTAAAGTACCGTCAGTATAT 595
QY 585 AATATTTTCACTGCGGTTTCTTAAGCAAAACCGCAGTCTAATGATATTTACACTAGCG 644
DB 594 AATATTTTCACTGCGGTTTCTTAAGCAAAACCGCAGTCTAATGATATTTACACTAGCG 644
QY 645 GGCTGCTAAAGAAACCGCCGCTTAAGATTTTACACTAGCGTTGGTGAACAACG 704
DB 534 GGCTGCTAAAGAAACCGCCGCTTAAGATTTTACACTAGCGTTGAACAACAACG 704
QY 705 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTAGTCTGACCTGGCGACATTAACAAACGTC 764
DB 474 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTAGTCTGACCTGGCGACATTAACAAACGTC 764
QY 765 AGTGAATAATAGCTCTAGATCGTCACTATAGAGCTTTCTATGTAAT 809
DB 417 AGTGAATAATAGCTCTAGATCGTCACTATAGAGCTTTCTATGTAAT 809

RESULT 10
CG455835 884 bp DNA linear GSS 17-SBP-2003
LOCUS PUIKG077DB ZM 0.6_1.0_KB Zea mays genomic clone ZM87A0602B13,
DEFINITION genomic survey sequence.
ACCESSION CG455835
VERSION CG455835.1 GI:34840835
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 884)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUIKG077DB

Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers

FEATURES
source
1..884
Location/Qualifiers

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A0602B13"
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COT selected genomic DNA library"

ORIGIN

Query Match 15.3%; Score 191.4; DB 29; Length 884;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGATGAGAGACAACATTTTCTAGAGTACTGTTTAAAGTACCGTCAGTATAT 584
DB 646 AACCGATGAGAGACAACATTTTCTAGAGTACTGTTTAAAGTACCGTCAGTATAT 588
QY 585 AATATTTTCACTGCGGTTTCTTAAGCAAAACCGCAGTCTAATGATATTTACACTAGCG 644
DB 587 AATATTTTCACTGCGGTTTCTTAAGCAAAACCGCAGTCTAATGATATTTACACTAGCG 528
QY 645 GGCTGCTAAAGAAACCGCCGCTTAAGATTTTACACTAGCGTTGGTGAACAACG 704
DB 527 GGCTGCTAAAGAAACCGCCGCTTAAGATTTTACACTAGCGTTGAACAACAACG 704
QY 705 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTAGTCTGACCTGGCGACATTAACAAACGTC 764
DB 467 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTAGTCTGACCTGGCGACATTAACAAACGTC 764
QY 765 AGTGAATAATAGCTCTAGATCGTCACTATAGAGCTTTCTATGTAAT 809
DB 410 AGTGAATAATAGCTCTAGATCGTCACTATAGAGCTTTCTATGTAAT 809

RESULT 11
BZ795791 889 bp DNA linear GSS 17-MAR-2003
LOCUS PUFQM22TB ZM 0.6_1.0_KB Zea mays genomic clone ZM87A014C19,
DEFINITION genomic survey sequence.
ACCESSION BZ795791
VERSION BZ795791.1 GI:28996519
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 889)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFQM22TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source

Location/Qualifiers
1. 889
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB2A314C19"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 15.3%; Score 191.4; DB 28; Length 889;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGTATGTGAGACACATTTTCATAGGTGTTTAACTACCGTCAGTGATTAAT 584
DB 420 AACCGTATGTGAGACACATTTTCATAGGTGTTTAACTACCGTCAGTGATTAAT 478
QY 585 AATATTTTCACTGGCGTTTCTTAAGCAACCGCCAGTGTATGATTTTACACTAGCG 644
DB 479 AATATTTTCACTGGCGTTTCTTAAGCAACCGCCAGTGTATGATTTTACACTAGCG 538
QY 645 GGCTGCTAAAGAAACCGCCGCTTAAGATTTTACACTAGCGGTGGTGAACAACG 704
DB 539 GGCTGCTAAAGTAAACCGCCAGTGTATGATTTTGAATGACGAGTGAACAACACCG 598
QY 705 CCTGTGAAAAAGCCGATTTCTTACTAGCCCTTACTGCTTGCACCTGACATTAACAAACGTC 764
DB 599 CCTGTGAAAAAGCCGATTTCTTACTGCGGCTTACGACTGAC---GGCAGTGAACAAATGCC 655
QY 765 AGTGAATAATAGCTCTAGATGCTGCTACTATAGAGCTTCTATGACT 809
DB 656 AGTGAATAATAGCTCTAGATGCTGCTACTATAGAGCTTCTGTTACT 700

3.

RESULT 12 891 bp DNA linear GSS 17-MAR-2003
LOCUS #BZ795799/c 891 bp DNA linear GSS 17-MAR-2003
DEFINITION PUF6M22TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMB2A314C19,
genomic survey sequence.

ACCESSION BZ795799
VERSION BZ795799.1 GI:28996535
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 891)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUF6M22TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source

Location/Qualifiers
1. 891
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/clone_lib="ZM_0.6_1.0_KB"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 15.3%; Score 191.4; DB 28; Length 891;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGTATGTGAGACACATTTTCATAGGTGTTTAACTACCGTCAGTGATTAAT 584
DB 670 AACCGTATGTGAGACACATTTTCATAGGTGTTTAACTACCGTCAGTGATTAAT 612
QY 585 AATATTTTCACTGGCGTTTCTTAAGCAACCGCCAGTGTATGATTTTACACTAGCG 644
DB 611 AATATTTTCACTGGCGTTTCTTAAGCAACCGCCAGTGTATGATTTTACACTAGCG 552
QY 645 GGCTGCTAAAGAAACCGCCGCTTAAGATTTTACACTAGCGGTGGTGAACAACG 704
DB 551 GGCTGCTAAAGTAAACCGCCAGTGTATGATTTTGAATGACGAGTGAACAACACCG 492
QY 705 CCTGTGAAAAAGCCGATTTCTTACTAGCCCTTACTGCTTGCACCTGACATTAACAAACGTC 764
DB 491 CCTGTGAAAAAGCCGATTTCTTACTGCGGCTTACGACTGAC---GGCAGTGAACAAATGCC 435
QY 765 AGTGAATAATAGCTCTAGATGCTGCTACTATAGAGCTTCTATGACT 809
DB 434 AGTGAATAATAGCTCTAGATGCTGCTACTATAGAGCTTCTGTTACT 390

RESULT 13 856 bp DNA linear GSS 17-MAR-2003
LOCUS BZ786431 856 bp DNA linear GSS 17-MAR-2003
DEFINITION PUGB229TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMB2A327F10,
genomic survey sequence.

ACCESSION BZ786431
VERSION BZ786431.1 GI:28980028
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 856)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUGB229TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source

Location/Qualifiers
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/strain="B73"
/db_xref="taxon:4577"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

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Best Local Similarity 81.8%; Pred. No. 2.8e-29;
Matches 233; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

OY	525	AACCGTAGTGGAGCAACATTTTCATPAGGAGTACTGTTTAAGTACCCTAGATATAT	584
Dd	144	AACCGCATGTGGAAACAATCTTTTACACGCGGTCTCCTTAAGCACCAACCATATATAT	203
OY	585	AATAATTTTCACATGCGGTTTTCTTAAGCAAACGCCAAGTCTAATGATATTACACTACCG	644
Dd	204	ATTATATTTTATATGCGGTTTTCTTTAAACAAACCGCACAGTCTAATATATTTAACACTGGTG	263
OY	645	GAGTCTTAAGAAAAACGCGCCGTGTGAAGAATTTTACACTAGCGGTGTGGAAACAATGTG	704
Dd	264	GTTCTCTTAAGAAAACCGTCAAGTATTAATGTATTATTACACTGGCTGTGGCAAAACAACG	323
OY	705	CCTGTGAAAAAAGCCGATTCCTACTACGCCCCCTAGCTTGCACTGGGCACATAAAAACGTC	764
Dd	324	CCTGTGAAAAAAGCCGATTTCTACTACGGCCCCCTA---ATACGTGTGGCACTGAAAAACGAC	380
OY	765	AGTGAATAATAGCTCTAGAGATGCTACTCTATTAGAAGCTTCAATATGACT	809
Dd	381	AGTGAATAATAGCTCTAGAGATGCTACTCTATTAGAAGCTTCAATATGACT	425

RESULT	14
CC014365	
LOCUS	
DEFINITION	CC014365 844 bp DNA linear GSS 31-MAR-2003 PUDHVO7D ZM.0.6.1.0_XB_zea mays genomic clone ZMMBT214B14,
ACCESSION	CC014365
VERSION	CC014365.1 GI:29398535
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 844)	
REFERENCE	Whitelaw C.A., Quackenbush J.J., Van Aken S., Uterback T., Renick A.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, V. and Bennerzen, J.
AUTHORS	Bennetzen, J.
TITLE	Maize Genomics Consortium
JOURNAL	Unpublished (2003)
COMMENT	Contact : Cathy Whitelaw

```

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white.law@tigr.org
Seq Primer: TP
Class: sheared ends.
Location/Qualifiers
1. 844
FEATURES
source

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FEATURES
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Db	332	AACCGATGAGAGATATCTTTTTCACAGCGGACCACTTAAAGACCCGTAAGTAAAT	391
QY	585	AATATTTTCACTAGCGGTTCTTTAAGCAAAACCGCAGGCTAAATGATATTTTACCTAGCG	644
Db	392	AATATTTTCACTAGTATTTCTTTAAAGTAAACCGCAGGCTAAATGATATTTTACCTAGCGG	451
QY	7045	GGCTGCTAAAGAAAACCGCCCGTGCTAAAGATATTTTACACTAGCGGTTGGTGAACAACCTG	7641

Accession	Sequence	Position
Db	452 GGCTGCTAAGAAAACACACAGTATATGTTATTTCACCTGGGGGTTGGGAACAACCG	5111
Qy	705 CTTGTAAAAAAGCCGATTCCTACTAGCCCTAGCTTGCACTGCGCAATPAAAAACGTC	7644
Db	512 CCTGTAAAAAAGGTGCATTTCTACTAGAACCCATAGC--ACTGGGGGCACTGGAAAAACGCC	5688
Qy	765 AGTGAATAATAGCTCTAGGATGCTGCACTPATAGAGCTTCATTAAGT	809
Db	569 AGTGCAAATAGCTTTAGAACGCCCACTTATAGAGCTTCGTGTACT	613

RESULT 15	
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LOCUS	
DEFINITION	CG132370 905 bp DNA linear GSS 21-AUG-2003 PUGB42TB ZM.0.6.1.0_KB Zea mays genomic clone ZMABTA0661H12, genomic survey sequence.
ACCESSION	CG132370
VERSION	CG132370.1 GI:34019817
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (pages 1 to 905)
Whitellaw,C.A., Quackenbush J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PU0GH42TD
Contact: Cathy Whitellaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white.law@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES	SOURCE	Location/Qualifiers
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		Cot selected genomic DNA library"

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Db	62	AACCGATGTGGAGTATCTTTTTCACAGGCGGACCACTTAAGACACCGCTGATTAAT	121
Qy	585	AATATTTTCACATGGCGTTTCTTAAGCAACCGGCAGTGTAAATGATATTTTACATAGCG	644
Db	122	AATATTTTTCACATGTGATTTCTTAAGTAAACCGGCAGTGTAAATGATATTTTACATGGCG	181
Qy	645	GGGTGCTAAAGAAAACCGCCCGCTGCTAAAGATATTTTCACTAGCGGTGGTGAAACAATG	704
Db	182	GGGTGCTAAAGAAAACCAACAGTATATATTTTACACTGGCGGTGGCAAAACAACG	241
Qy	705	CCGTGTAAGAAAAGCGATTCCTCACTAGCGCCCTTACCTGGCACTAGGCGCATTAAGAAAAGTC	764
Db	242	CCTGTAAAGAAAGGTGCAATTTCTACTGACCACTAGC---ACTGGCGGCACTGTGAAAACGCC	298
Qy	765	AGTGAATAATAGCTTAGAGTGCATCACTAATAGAGCTTCTATGTACT	809

DB 299 AGTGC AATAGCTCTAGGACTGCCCATATATAGACTTCTGTACT 343

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